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Title:
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Listing first 45 summaries
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      Result
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Query
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

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ocus	DNA TIMEGE
EFINITION	Sequence 22 from Patent W00177356.
CCESSION	AX280988
ERSION	AX280988.1 GI:16608262
EYWORDS	•
OURCE	Physcomitrella patens.
ORGANISM	Physcomitrella patens
	Eukaryota; Viridiplantae; Streptopnyta; Embryopnyta; Bryopnyta;
	Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrelia.
EFERENCE	1 (sites)
AUTHORS	da costa e Silva,O., Bohnert,H.J., van Thielen,N., Chen,K. and
	Sarria-Millan,R.
TITLE	Protein kinase stress-related proteins and methods or use in plants
JOURNAL	Patent: WO 0177356-A 22 18-OCT-2001;
	BASF Plant Science GmbH (DE)
EATURES	Location/Qualifiers
source	12177
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	/db_xref="taxon:3218"
ASE COUNT	522 a 508 c 547 g 600 t
RIGIN	

Qy 841 catacgaaacgagggcccagagcctcactcgctggagaccgacc	661 gccaaatgcccaacctttcttagaacgtcagccgaaggtagtacatcgaggatccaaga [	481 tytccgggtggtctaccccgacggccacgtcgagaatctgagcaaatcttgtagcgtgc	241 301 301 361 361 421 421	ygagcaggctgagagttcggcagcgaagttacactcgacctggctga	Query Match Best Local Similarity 100.0%; Score 2177; DB 6; Length 2177; Best Local Similarity 100.0%; Pred. No. 0; Matches 2177; Conservative 0; Mismatches 0; Indels 0; Gap Matches 2177; Conservative 0; Mismatches 0; Indels 0; Gap Mismatches 0; Indels 0; Gap Oy 1 atcccgggcttgtattggctcggataatttatgttgacaattgattg
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                                            GAAGCCTGTCATGGAATTCCACACTCCGATGGCTTACCGGGATAGTGGGTCTCCGCCGAA
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             tttgtagcgcggactgcg-tcgaagtattctgctgcatctcagcaagttcaacgaaatcg
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TTTGTAGCGCGGACTGCGATCGAAGTATTCTGCTGCATCTCAGCAAGTTCAACGAAATCG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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nt: WO 0177356-A 9 18-OCT-2001;
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Holmes, S.E., O'Hearn, E., Rosenblatt, A., Callahan, C., Hw
Ingersoil-Ashworth, R.G., Fleisher, A., Stevanin, G., Brice
Potter, N.T., Ross, C.A. and Margolis, R.L.
A repeat expansion in the gene encoding junctophilin-3
associated with Huntington disease-like 2
Nat. Genet. 29 (4), 377-378 (2001)
                                                                                       l Similarity 8.18
36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical Institutions, 600 N. Wolfe St., Baltimore, MD 21287, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Holmes, S.E., Ingersoll-Ashworth, R.G.,
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/HGFEVLGGYYTWPSCGTYQGTWAQGKRHGIGLESKGKWYYKGEWTHGFKGRYGVRBCAG
NGAKYEGTWSAGLOGSYCTETYSDG
NGAKYGTWSAGLOGSYCTETYSDG
NGAKYGTWSAGLOGSYCTETYSDG
NGAKYGTWSAGLOGSYCTETYSDG
NGAKYGTWSAGLOGSYCTETYSDG
NGAG
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/note-"isolated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(<36507. .>36887)
/gene="JPH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membrane and endoplasmic reticulum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<36507. .36887)
/gene="JPH3"
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/db_xref="taxon:9606"
/chromosome="16"
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                                                                                                                 8.1%;
                                                                                %; Score 46.6; I;
; Pred. No. 0.03;
230; Mismatches
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AC099664/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1953 ttcgggctttgtttcgagctcatgtaccatcgactagcgtcactttgactgcggtgataa 2012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WBRDSHHMMYDSMARMACMGMV 61060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDSKGMKWCKMYGSWSKKHHCWCBWGWCDBYBATWGTKSTCSDBGYSYSWTDDHMHSRWB 61038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WKWKWVHYHVHWBWSRWVHDVVDHWMKDVWCHWKWSRSWVKCHWGYCMTGKWBHDDYHYW 60978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aacatagtgcttcacttctgggttgttcaccactaggatcatatgaccttctcatctatt 1952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attgtctttcctatgtagaacatagcgaggacacttgcgcctggtgggcacatcccatag 1892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WKWKGGTKARWYYYSKTYTCTMYTWRMWWKKYWRMWWTWWKYYCWKTKYKKYGGKGSSYM 60738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tgagcgcagatcttgcttccgcagtttgtttcataacgttttggttcgtagggggcctag 1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgctgtttacaagatagcggca 2094
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On !
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1 (bases 1 to 157442)

Kaul,R.K., Olson,M.V., Raymond,C. and Haugen,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unordered pieces.
AC099664 AC012585
AC099664.1 GI:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bmitted (17-NOV-2001) Genome Center, University of Washington, x 352145, Seattle, WA 98195, USA
NOV 17, 2001 this sequence version replaced gi:13194374.
                                    Sequencing vector: unknown; 44% of reads sequencing vector: plasmid; L08752; 56% of reads Chemistry: Dye-terminator EI; 89% of reads Chemistry: Dye-terminator Big Dye; 11% of reads Assembly program: Phrap; version 0.990319 consensus quality: 155430 bases at least Q30 Consensus quality: 15670 bases at least Q30 Consensus quality: 157102 bases at least Q30 Consensus quality: 15710
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                                                                                                                                                                                                                                                                                                                                                                                   Center project name: chr-3
Center clone name: RP11-6B4 (bc0602)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: University of Washington Genome Center Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.genome.washington.edu
                                                                                                                                                                                                                                                                                                                                                     ----- Summary Statistics
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              sum-of-contigs
                                                                  REFERENCE
AUTHORS
TITLE
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Best Local Similarity 48.4%;
Matches 119; Conservative
                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48966 ATAATC 48961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49086 TATCTTTTGTGCATATACTATAGGTTTTTGCTTTGTGGTTACCATGAGGCTTACATAAAA 49027
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49026 CATGCTATACTAAAAACAGGGGGCTTTACACCAATAACAACTTAACTTTGATTGCATAAA 48967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2011 aatcgtttgtcaatttagtggagctttgtagattgatagattgccatttgtacagtagcttg 2070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1951 ttttcgggctttgtttcgagctcatgtaccatcgactagcgtcactttgactgcggtgat 2010
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                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens chromosome 3 clone SEQUENCE, 17 unordered pieces. ACO24967 ACO24967.4 GI:13959248 HTG; HTGS_PHASF1. umra re---
2 (bases 1 to 183978)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183978)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens chromosome 3, clone RP11-554B18
                                                                                                   Homo sapiens chromosome Unpublished
                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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65505. .157442
/note="assembly_name:Cont1g36"
a 28472 c 27460 g 50919 t
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/db_xref="taxon:9606"
/chromosome="3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA linear HTG 07-MAY-2001 RP11-554B18 map 3, WORKING DRAFT
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COMMENT

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100 others

Length 157442; Indels

0; Gaps

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Locus

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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., Mihova, T., Mianda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Rochen, C., Schamer, S., Carcare, B., Carcare, R., Carcare, R., Carcare, R., Carcare, L., Carcare, 
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L6081
Center clone name: 554, B.18
Center clone name: 554, B.18
Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 177205 bases at Least Q40
Consensus quality: 180493 bases at Least Q30
Consensus quality: 180493 bases at Least Q20
Insert size: 183000; agarose-fp
Insert size: 18378; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     runs of \hat{N}, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 5.1 in Q20 bases; agarose-fp Quality coverage: 5.1 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Whitehead Institute/ MIT Center for Genome Center code: WIBR
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an,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
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13691 14794: contig of 1104 bp
14795 14894: gap of 100 bp
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                                                                    20619: gap of 100 bp 26197: contig of 5578 bp in length 26297: gap of 100 bp 35892: contig of 9595 bp in length 35992: gap of 100 bp
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20519: contig of 1586 bp in length
92: gap of 100 ap
46225: contig of 10233 bp in length
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16129: contig of 1235 bp in length
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COMMENT

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ORIGIN
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Best Local Similarity 48.4%;
Matches 119; Conservative
                                49689 AGAACTTACTACTGCATTTGTTATTTTCTTCCTGGTTATTTTGTATGTCCTTTATTCCTC 49748
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                                                               1891 agaacatagtgcttcacttctgggttgttcaccactaggatcatatgaccttctcatcta 1950
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111142 11241: gap of 100 bp
111242 127337: contig of 16096 bp
127338 127437: gap of 100 bp
127438 144980: contig of 1743 bp
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172868 183978: contig of 11111 bp in length
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98925, .111141
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26298. .35892
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/db_xref="taxon:9606"
/chromosome="3"
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17431. .18833
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/clone_lib="RPCI-11 Human Male BAC"
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127438. .144980
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46326. .85357
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85357: contig of 39032
85457: gap of 100 bp
98824: contig of 13367
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32376 c 32914 g
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|3691. .14794
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145081. .172767
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ju: gap of
172767: r-
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                                                                                                      Mismatches
                                                                                                                      Score 42.8;
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Best Local Similarity 3.1%, pred. No. 0.64;
Matches 11; Conservative 199; Mismatches 148; Indels
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Homo saptens chromosome 17 cione RP11-428023 map 17,
SEQUENCE SAMPLING.
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Dorner, F., Scheiflinger, F. and Falkner, F. Gunter.
Recombinant fowlpox virus
Patent: US 5670367, A 14 23-SEP-1997;
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Sequence 14 from patent US 5670367.
166494
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AUTHORS
TITLE
JOURNAL
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; """

Mammalia; Eutheria; Primates; \"\"

1 (bases 1 to 70203)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Birren,B., Linton, D., Clone RP11-428023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (25-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A.,
Camarata, J., Campoplano, A., Chang, J., Cheepel, Y., Colangelo, M.,
Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This record contains 84 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                be preserved.
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755 854: gap of 100 bp
855 1623: contig of 769 bp in length
1624 1723: gap of 100 bp
1724 2471: contig of 748 bp in length
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                            6816: gap
of 703 b, 100 bp 103 bp 100 bp 100 bp 100 bp 100 bp 100 bp 100 bp 106: gap of 706 gap of 706: gap of
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12822: gap of 100 bp 10 103530 13629: gap of 100 bp 103530 13629: gap of 100 bp 103630 1458: contig of 729 bp in 14359 14458: gap of 100 bp 10458: gap 10458: gap of 100 bp 10458

12010: gap of 1 12722: contig of

100 bp of 712 bp in : 100 bp of 707 bp in :

11133: 10274:

133: gap of 100 bp 11910: contig of 777 bp 74: gap of 1 11033: contig of

bp in ni dq bp in in

100 bp f 759 bf

1 17003; gap of 100 bp 17752; contig of 749 bp in 3 17852; gap of 100 bp 1876; contig of 724 bp in

16149: 15338:

4458: gap of 100 bp 1528: contig of 780 bp in 1638: gap of 100 bp 1649: contig of 711 bp in 1649: gap of 100 bp 1649: gap of 100 bp 16903: contig of 754 bp in 16703: gap of 100 bp 1752: contig of 749 bp in 16782: contig of 7492 bp in 167

8449: contig of 752 b 10 8549: gap of 100 bp 10 9312: contig of 763 b 3 9412: gap of 100 bp 1 1074: contig of 762 b

dq E.

7 7597: contig ( 8 7697: gap of 8 8449: contig c 0 8549: gap of

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of 781 bp in 1 100 bp of 752 bp in

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KEYWORDS
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Similarity 58.3%;
70; Conservative
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40430 41154: contig of 725 bp in le
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41155 41254: gap of 100 bp
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43657 43756: gap of 100 bp
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53628 53727; gap of 100 bp

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54583 55325; contig of 743 bp

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6, complete
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77 18676 gap of 7100 bp 11 1995; contig of 719 bp in 1e 96 1945; gap of 100 bp 6 20253; contig of 758 bp in 1e 54 20153 gap of 100 bp 100 21917; contig of 746 bp in 1e 100 2199; gap of 100 bp 100 21917; contig of 718 bp in 1e 100 21917; contig of 718 bp in 1e 100 21918; gap of 100 bp 10 1e 100 22017; gap of 100 bp 10 1e 100 22018; contig of 711 bp in 1e 100 2358; contig of 711 bp in 1e 100 24318; contig of 720 bp in 1e 100 24318; contig of 720 bp in 1e 100 24318; gap of 100 bp 100 24318; gap of 100 bp 100 25180; gap of 100 25180; gap of

length

length length

10 26109: gap of 100 bp in le 2665: contig of 756 bp in le 66 26965: gap of 100 bp in le 66 27745: contig of 780 bp in le 66 27745: contig of 780 bp in le 2856: gap of 100 bp in le 2856: gap of 100 bp in le 57 28656: gap of 100 bp in le 57 29414: contig of 758 bp in le 15 30240: contig of 726 bp in le 15 30240: contig of 726 bp in le 10 31209: gap of 100 bp in le 10 31209: gap of 100 bp in le 30 32039: gap of 100 bp in le 30 32752: contig of 720 bp in le 53 32852: gap of 100 bp in le 54 33653: gap of 100 bp in le 54 33653: gap of 100 bp in le 54 33653: contig of 779 bp in le

0;

53 35226: contig of 764 k 27 35336: gap of 100 bp 27 36088: contig of 762 k 27 36088: gap of 100 bp 36927: contig of 739 b

f 764 bp 100 bp f 762 bp 100 bp f 764 bj

ij ij

length length

37027: gap of 37761: contig

3 32852: gap of 10 33533: contig of 7 44 33653: gap of 10 44 3452: contig of 7 3 34462: gap of 10 3 35226: contig of 7

length length

length

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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EmBL: Sw., SWISSPROT: Tr., TREMBL: Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 153072)
Wall,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORTANT: This sequence is not the entire insert of clone RP11-344F20 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-344F20 is at 133072 in this sequence. The true right end of clone RP11-505K1 is at 100 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    requests: clonerequest@sanger.ac.uk
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/db_xref="taxon:9606"
/chromosome="6"
/clone="RP11-344F20"
/clone=lib="RPCI-11.2"
60. .177
                                                                                                                                                                                                                                                                           /note-"MLTlH repeat: matches 33. .541 of 6051.\ .6176
                                          /note-"L1PA5 repeat: matches 5184.
11814. .14211
                                                                                          /note="MLT1A1 repeat: matches 12. 8872. .9833
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                                                                                                                                                          /note="48 copies 2 mer ta 69% conserved"
                                                                                                                                                                                                                                                                                                                                                                                      'note="37 copies 2 mer ac 91% conserved"
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1068. .1143
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                      repeat: matches 3692.
                                                                                                                                                                                                                                                                                                                                           .310 of consensus*
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                      .6120 of consensus
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/note="L2
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/note="LIMD2 repeat: matches 5494. .5968 of consensus"
18607. .18978
                                                                                                            /note="MER96 repeat: matches 115. .172 of consensus" 34150. .34490
                                                                                                                                                                                                  /note="MER6B repeat: matches 32098, .32360
                                                                                                                                                                                                                                                     /note="L1MEc repeat: matches 1738. .1988 of consensus"
31891. .32097
                                                                                                                                                                                                                                                                                                                                           /note="THEIB repeat: matches 15. .364 of consensus"
30733. .31170
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                                                                                                                                                                                                                                                                                                                                                                                                          consensus'
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25079. .25177
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'note="MIR repeat: matches 49.
                                                                                        'note="MER7A repeat: matches 1.
                                                                                                                                                                              note-"LIMEc repeat: matches
                                                                                                                                                                                                                                                                                                                    note-"LlMA8 repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="25 copies 2 mer tt 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note∞"L1PA12 repeat: matches 4063. .4405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note-"L1MD2 repeat: matches 5951. .6321 of consensus"
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-e="IIPA12 repeat: matches 4405. .6153 of consensus"
)8. .24802
                    MIR repeat: matches 31. .41312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i8 copies 2 mer tt 88% conserved"
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.17526
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.124 of consensus
                                        .250 of consensus"
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RESULT
AC025870
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Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 162508)
                                                                                                                                              AC025870 162508 bp DNA
Homo sapiens clone RP11-25P4, WORKING I
                                                                                   pieces.
AC025870
AC025870.2 GI:10198533
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                     Homo sapiens
                                                                     uman
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61297..614
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/note="L1PA16 repeat:
42251. .42816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER5A repeat: matches 4. 57070. .57366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER33 repeat: matches 2. 55720. .55804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 1. .306 of consensus"
53737. .54225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="L2 repeat: matches 2430.
45231. .45525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2461. .2494 of 44633. .44731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 1885.
43827. .44123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="L2 repeat: matches 1432. .1586 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2619. .2727 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="L1PA3 repeat: matches 6027. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="L1PA15 repeat: matches 5547. .6153 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="MER5B repeat: matches 1. .178 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="11MB3 repeat: matches 5762. .6184 of consensus"
52294. .52599
                                                                                                                                                                                                                                                                                                                                                                                               1.8%;
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.55708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AluY repeat: matches 6. .300 of consensus, .59895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat: matches 1391. .1699 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                copies 2 mer tc 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat: matches 12. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                               Score 40; DB 9; Length 153072; Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              matches 2431.
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                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                     linear H
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E, 42 unordered
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JOURNAL
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S Birren, B., Linton, I., Nusbaum, C. and Lander, E.

Unomblished

Linton, I., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Boddes, S., Donino, M., Dolle, H., Serreira, P., Fittheyn, W., Goge, D.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dikar, J. S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Minder, S.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Minder, J.,

Boddes, S., Donino, M., Dolle, M., Serreira, P., Fittheyn, W., Goge, D.,

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Horland, J.C., Lilev, L., Dolley, J., Serreira, P., Kann, L., Karatas, A.,

Horland, J.C., Lilev, L., Dolley, J., Brerreira, P., Kann, L., Karatas, A.,

Horland, J.C., Lilev, L., Dolley, J., Warder, C., Kann, L., Karatas, A.,

Horland, J., Gardyna, S., Ginde, S., Goyette, M., Gore, J.,

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Horland, J., Gardyna, J., Gardyna, J.,

Feder, J., Horland, J., Warder, G., Merga, J., Worrow, J.,

Horland, J., Gardyna, J., Warder, G., Menga, V., Worrow, J.,

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Horland, J., Warder, J., Warder, J., Warder, J., Worrow, J.,

Horland, J., Warder, J., Warder, J., Warder, J., Worrow, J.,

Horland, J., Warder, J.,
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21263:

31457:

27497: 25694:

29430:

BAC"

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33461 33460: gap of 100 bp
33461 36064: contig of 2604 bp in length
36065 36164: gap of 100 bp
36165 37979: contig of 1815 bp in length
37980 38079; gap of 100 bp
40464 40563: gap of 100 bp
43575 46574: gap of 100 bp
45564 43574: gap of 100 bp
45564 43574: contig of 1585 bp in length
45760 45259: contig of 1585 bp in length
4560 45359 gap of 100 bp
47486 47485: gap of 100 bp
47486 4979: contig of 2026 bp in length
49680 4979: gap of 100 bp
47486 51919: contig of 2040 bp in length
51920 51919: contig of 2040 bp in length
55271 5370: gap of 100 bp
55271 5370: gap of 100 bp
55271 5370: gap of 100 bp
61670 61669: gap of 100 bp
61670 65776: contig of 2853 bp in length
65777 68164: gap of 100 bp
65776 68264: gap of 100 bp
65776 68264: gap of 100 bp
65776 72331 72430: gap of 100 bp
657877 75821: gap of 100 bp
67231 72330: contig of 3291 bp in length
75822 79327: contig of 3291 bp in length
75823 79470: contig of 6743 bp in length
79428 66170: contig of 6743 bp in length
79428 76470: contig of 6743 bp in length
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125856 133343: contig of 7488 bp in length
133344 133443: gap of 100 bp
                                                                                        162035 162134: gap of
162135 162508: cont
                                                         Location/Qualifiers
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25594: contig of 1204 bp in
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125755; c
'85"
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141679; cont
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62034: contig of 8268
                                                                                                                                                                                    1443: gap of 100 bp
141679: contig of 8236 bp
1779: gap of 100 bp
153666: contig of 11887 b
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33360: contig of 1903 bp in length
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29330: contig of 1833 bp in
30: gap of 100 bp
31357: contig of 1927 bp in
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AC022797
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                                                                                                                                                                                                                                                                                                                        DEFINITION
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Best Local Similarity 58.3%;
Matches 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88889 ATTAATGTTTTTAGCTCAATTATCTGTGACAAGGATCACTTCGCAGCTTGGGTGAATTGT
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 174200)
Eirren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 6, clone RPll-281Gl3
Unpublished
                                                                                                                                                                                                                                                                    AC022797
                                                                                                                                                                                                                                                                                     AC022797 174200 bp
Homo sapiens chromosome 6 clone
SEQUENCE, 22 unordered pieces.
                                                                                                                                                                                                           AC022797.3 GI:7249244
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27498 .29330
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22755. .24290
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1. .1133
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/note="assembly_fragment"
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43675. .45259
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/note="assembly_fragment"
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dewar, K., Dewar, K., Domion, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Garders, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McFernan, K., McPheeters, R., Meldrin, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Zimmer, A., and Sody. M., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
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Center clone name: 281_G_13

Center clone name: 281_G_13

Sequencing vector: M13; M77815; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: 100% program: Phrap; version 0.960731

Consensus quality: 163082 bases at least Q30 consensus quality: 169787 bases at least Q20 consensus quality: 179797 bases at least Q20 Insert size: 182000; agarose-fp Insert size: 172100; sum-of-contigs Quality coverage: 3.6 in Q20 bases; sqarose-fp Quality coverage: 3.8 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                      1 3194: contig of 3194 bp in length
3195 3294: gap of
3295 5894: gap of 100 bp
5795 5894: gap of 100 bp
5895 9861: contig of 3967 bp in length
9862 13464: contig of 3967 bp in length
13465 13564: gap of 100 bp
13565 15205: contig of 1641 bp in length
15206 15305: gap of 100 bp
15306 19909: contig of 4604 bp in length
19910 2009: gap of 100 bp
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13565. .15205
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29119. .34619
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128799: gap of 100.
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57620: config of 14432 h
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Homo sapiens junctophilin 3 (JPH3)
AF429315
AF429315.1 GI:17646244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 125020)
Holmes, S. E., Ingersoll-Ashworth, R.G., Ross, C.A. and Margolls, R.L.
Direct Submission
Submitted (05-OCT-2001) Psychiatry, Johns Hopkins Medical
Submitted (05-OCT-2001) Baltimore, MD 21287, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 125020)

1 (bases) to 125020;

1 (ba
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /map="16q24.3; between D168520 and WI-12410"
/note="1solated from a patient with Huntington's
Disease-Like 2 (HDL2)"
complement(35581. .35746)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128800. .143088
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                                                                                                                                                                                                                                                                                                                                                                            complement(<36507. .>36887)
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Pred. No. 3.6;
0; Mismatches
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BASE COUNT
ORIGIN
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Query Match Best Local Sim Matches 131;

Similarity 12.0 31; Conservative

1.8%; Score 38.6; D 12.0%; Pred. No. 9.3; tive 449; Mismatches

DB 9; 506;

Length 125020;

Gaps

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Š В 밁 В Š В 밁 δÃ 밁 Ş 밁 Ş В δÃ 밁 Q 밁 Q B δÃ DЪ Qy Вb Ş 밁 δÃ DЬ Š 51021 51139 WWTSSMACMYWYKGSRRKTKSMATSGCMRMGAM--RSKGGMRKYWSCRYKGMRWGRWSGY 51082 51259 51319 YMRWCCTCMARAMWRARMAAMRRARMAGAARAWMSMWMWSMMMRBHAAAMMARMWAAAK 51260 51379 YAKGSAGWRWGSYKWGAWYSCRMSASKKSRMTCYWSCCCTSCKGCYWMYWSWKYGAGMCW 51320 51439 51499 AAAMSMCGTCYMKMCTRRMMATACAWRRWRAWWMSCCMRKCWTSKWSKMGRRMRYCWSWA 51440 51557 51617 51677 WTKRRGWGRTRKAAAWCAKCCWWMYRCTGMCWAKTYYATWYKSWKSRWTTGWRRMGTRRA 51618 51737 51797 1044 745 445 207 327 267 aagctcgacgagtttcaatcgaacgtagagttttagtcggggtcgaggatctatgtatccg 326 YCTCWGGRMCKGMKSSCCASRSGCKSYKMAGSWRCRGRRGMSCWYWSSMKSYSMASYKSS 50962 KGCSGYMSMGMYGSGRTSKYCSYTGGYCSKCSAKMCKSKSTSKSCCTKSKYSCSMGRYSS 51022 ctcacctcgctggagaccgaccgatcgaagcaccttaagctcgttttcattcggcattgct 923 WYCYSSMYAARRMGTYSGGKKRKWASTSCMCCCRRGCCMKKKGMRWCSTTYTGMSGGKSR 51140 RWMYYAGSYMSKCRSRWGGYKGRSRSRSGMSWRTRGYSYSARCYMSKSAGGAGKCKGAGS 51380 SYWWCASYYSRWRGSAWSYWAGGYTSYRKGSWGWGKMYKGSRARGSMSRWSKRSWWKKSW tttccggagaggccttatcgccgacggcaactgccaaagacgagattactcagatgatac 1043 tgcgagcacttcgacttcctagaatttcaatagacctaatggaatcgccactccctaatc 983 tgattatcattcagtaacgatgcagcagctt-gaatccatacgaaacgagggcccagagc 863 CWWWYSYRKYCWMSMMMASWAAMAMWMMCTAAWYYKKWTRMRRWSKYSSSYAYAWYATMC 51200 ggtccatgtgcgggagttgcgaagcccgacgcatgggagccaacagtcacggaaggtttt 804 acgtcagccgaaggtagtacatcgaggatccaagattttgccacgattttccaaacatgg 744 gctcgagtatggggtgacctacttcgtttgcgcaacgccaaatgcccaacctttcttaga ctactatgtctgcggtagcaccccttacacaatcaccaatcgtatggcagcggaagaggt 624 ccacgtcgagaatctgagcaaatcttgtagcgtgcacgatcttcttctgggtaatccaga MAKSCMRRYMMYKWGGGAGKCCSAGGMTGRTGS--RWSACCWKMSKKSASKARYAYASTG tctcactccgttttcttgtgtcacggttcaaggttatgtccgggtggtctaccccgacgg WMWWWYWKKYYRARMKCAKTRSMWMASKYSKSYARKCCSMWSAYKKYKSRASRCKGWGK 51558 gaggtggaccgcatcagaactatttattccttgtgagggaaggatcgaggttccaatggg 444 SARRAAMYRSCSKGRRRGKKKSSKGGGRGGKKWMASMTYSKRCCAKSTGRRRGGTKGSSC 51678 RKGRSRASARWKSYSCASRRKSCWRMMRGCSYMTGRSSMGTMSKRKGSRTSMGSKAGTYR 51738 atttaggggcaccaccggtttgttggagtcccttgccacttattacaattgttggtttac 266 504 51500 51798

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Jimmer A., Vassiliev H., Vo A., Wheeler J., Wu X., Wyman D., Ye W.J.,
                                                                                                                                                                On Mar 30, 2000 this sequence version replaced gi:6532098. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                 Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Last updated, Version
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                                                                                                                     MIT Center
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                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases.
for Genome Research, 320 Charles
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Best Local S
Matches 89
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Chemistry: Dye-terminator Big Dye; 1100% of
Assembly program: Phrap; version 0.960731
Consensus quality: 151809 bases at least (
Consensus quality: 153406 bases at least (
Consensus quality: 154041 bases at least (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 5.5 in Q20 bases; agarose-fp Quality coverage: 5.6 in Q20 bases; sum-of-contigs
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Insert size: 154642; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33705 45042: contig of 11338 bg
45043: contig of 11338 bg
45043 45142: gap of 100 bp
45143 77339: contig of 32197 bp
77340 77439: gap of 100 bp
77440 155542: cont.
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be
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16232 21713: contig of 5482 t
21714 21813: gap of 100 bp
21814 25983: contig of 4170 t
25984 26083: gap of 100 bp
26084 33604: contig of 7521 t
33605 33704: gap of 100 bp
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3919 4018: gap of 100 bp
4019 7852: contig of 3834 bp in length
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 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    it is available and the accession number will
                                                                                    В₽;
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                1.8%;
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pred. No. 9.7;
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RESULT 12

AC0136

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RP 1-15

Unpublished. Birren

n B., Lint sapiens,

clone

RP11-10L7";

Linton

-155542

Eutheria;

Primates;

-155542

Homo sapiens (human)

HTGS\_DRAFT;

HTGS\_PHASE1

RP11-10L7,

Center cod Web site:

Center: Whitehead Institute/

code: WIBR

http://www-seg.wi.mit.edu

Project Information

Submitted Zimmer

Institute/MIT Center

MA 02141,

USA

Zody M.;

Center project name: L3101 Center clone name: 10\_L\_7

Statistics

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Gaps

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                                                                                                                                                                                                                                                             Sequencing vector: M13; 53%
Sequencing vector: M13; 53%
Sequencing vector: M13; 53%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 156775 bases at least 040
Consensus quality: 157110 bases at least 030
Consensus quality: 157210 bases at least 020
Insert size: 155000; agarose-fp
Insert size: 157371; sum-of-contigs
Quality coverage: 10.23 in 020 bases; sum-of-contigs
Ouality coverage: 10.21 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (15-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Feb 7, 2002 this sequence version replaced gi:18151028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drafting center: WIBR
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AC107067 AC013612
AC107067.2 GI:18584834
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Waterston, R.H.
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Unpublished
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Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 156325)
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                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of I contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                               be
                                                                               preserved
                                   Location/Qualifiers
∕organism⇔"Homo sapiens'
                     .156325
                                                     156325: contig of 156325 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-NOV-2000) DOE Joint Genome Institute, 2800 Norive, Wainut Creek, CA 94598, USA On Nov 26, 2000 this sequence version replaced gi:8575922. Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-AUG-1999) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 162914)
                                                                                                                                                                                                                                               SHGC-56762 G37043
SHGC-57254 G38378
                                                                                                                                                                                                                                                                                                                                                    www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (basea 1 to 162914)

DOB Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                          Quality: Phrap Quality >=40 99.68 of Sequence: Estimated Total Number of Errors is 0.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                    WI-11361 G24462.
                                                                                                                                                                                                         SHGC-89248 G61707
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                                                                                                                                                                                                                                                                                           STS Content:
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45699 a 32863 c 31085 g 46678 t
                                     42170 a
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/chromosome="4"
/clone="RP11-10L7"
1, .156325
                                                                                                                                          Location/Qualifiers
1, .162914
                                   /chromosome="19"
/clone="CTD-2102P23"
36675 c 37407 g 46662 t
                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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ne 19 clone CTD-2102P23, complete sequence.
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DOE Joint 1 94598, USA

26-NOV-2000

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Db 105236 GGGCTGTTTTATAGGATTTGGGTACATAAAGGAAAATTACAGTCAAAGGGGGTTGTTCTC 105295
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Center project name: MAKF
Center clone name: MAKF
Center clone name: RP27-243F9
Center clone name: RP27-243F9
Center clone name: RP27-243F9
Chemistry: Dye-terminator Big Dye: 18% of reads
Chemistry: Dye-terminator Big Dye: 18% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 80612 bases at least 040
Consensus quality: 101873 bases at least 030
Consensus quality: 101873 bases at least 020
Estimated insert size: 97280; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 14, 2001 this sequence version replaced gi:10122026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fernandez,C., Ferraguto,D., Forcum Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M., Hosak,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,J., Kelly,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morris,S., Neal,D., Nelson,A., Nguyen,R., Nguyen,R., Oguh,M., Parish,B., Neal,D., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 69507)

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Davis, C., Dejado, O., Ding, Y., Dugan, Rocha, S., C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Dejado, O., Ding, Y., Dugan, Rocha, S., Cox, C., Dejado, O., Ding, Y., Dugan, Rocha, S., C., Carlos, C., C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 69507)
                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTGS_PHASE1.
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h

*NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "working draft' sequence. It currently

* consists of 25 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                        20847
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                                                                                                                                                  /clone="RP23-243F9"
12392 c 12647 g
                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="2"
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            1.7%; 51.5%;
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REFERENCE AUTHORS

AC079266

DEFINITION

ACCESSION VERSION

SOURCE ORGANISM KEYWORDS QΥ

Matches Query Match Best Local

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pu and is derived by analysis of the total score distribution. s of printed

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1.6	1.6	1.6	1.6	1.6	1.6	1.6	24.8	100.0	% Query Match Length DB
14458	7581	7201	3612	2625	5845	5059	683	2177	Length
23	23	23	21	22	24	20	24	24	DB :
ABL10220	ABL10234	ABL05860	AAZ51921	ABA15017	ABL32301	AAX84332	ABA91064	ABA91077	Q1
Drosophila melanog	Drosophila melanog	Drosophila melanog	N. tabacum Nhrl ge	Human nervous syst	Human immune syste	Stealth virus nucl	Physcomitrella pat	Physcomitrella pat	Description

AAS46415 AAZ60929 AAK61399
AAS8/44/ AAH24065 ABL32645
AAC77413 AAF18176
AAS60944 AAS60945
AAS60257 AAS60257 AAF21692
AAS60619
AAZ16544 AAS60258
AAI61373 AAH54179
AAK89550 AAK89551
AAS62323
ABA91140
ABA91113 ABA91139
AAS45411
ABL15898
ABL33078 AAX20257
AAA10595
ABL34445
ABL32988
ABL32087

## ALIGNMENTS

Physcomitrella patens MPK-3 full-length cDNA, 22-FEB-2002 ABA91077; ABA91077 standard; cDNA; 2177 ب (first entry) BP.

SEQ ID

NO:22.

Protein kinase stress-related protein; PKSRP; moss; protein kinase-6; PK-6; protein kinase-7; PK-7; protein kinase-8; PK-8; protein kinase-9; PK-9; casein kinase homologue-1; CK-1; casein kinase homologue-3; CK-2; casein kinase homologue-3; CK-3; mitogen-activated protein kinase; MAP kinase-2; MPK-7; MAP kinase-3; MPK-3; MAP kinase-4; MPK-4; MAP kinase-5; MPK-5; calcium-dependent protein kinase-1; CPK-1; calcium-dependent protein kinase-1; CPK-1; calcium-dependent protein kinase-1; CPK-2; overexpression; environmental stress; salinity; drought; temperature; tolerance; environmental stress; salinity; drought; temperature; 07-APR-2000; 2000US-196001P 06-APR-2001; 18-OCT-2001. WO200177356-A2 Physcomitrella patens. transgenic plant; 2001WO-US11435 expressed sequence tag;

(BADI ) BASF PLANT SCI GMBH

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CC Sequences AAM52830-AAM52842 represent novel protein kinase stress-related CC proteins (PKSRPs) from the moss physcomitrella patens, and sequences CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA CC sequences were obtained from expressed sequence tags (ESTs; ABA91056-CC ABA91069) derived from Physcomitrella patens cDNA libraries. The PKSRPS CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (CK-7), protein kinase-8 (PK-0), protein kinase-9 (PK-9), casein kinase-1 (CK-7), protein kinase-1 (CK-7), protein kinase-2 (CK-2), casein kinase-1 (CK-7), protein kinase-1 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2), CC calcium-dependent protein kinase-1 (CFX-1), and calcium-dependent protein confer conference to environmental stresses such as salinity, drought, cumperature, metal, chemical, pathogenic and oxidative stress.

CC temperature, metal, chemical, pathogenic and oxidative stress.

CC transgenic plants and seeds with increased tolerance to salinity drought cand temperature. The transgenic plants generated can be monocots or calcium-dependent protein structural studies and temperature. Solution, rapeseed, cassava, sunflower, tagetes, leguminous plants (e.g., soybean, peanut, Vicia species, alfaffa), solanaceous plants (e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea, complex structural studies and as markers for specific regions of the genome.
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                                                                   plant;
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                                         patens.
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CS Sequences AAM52830-AAM52842 represent novel protein kinase stress-related CC ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA CC ABA91089 derived from the moss physcomitrella patens, and sequences CC ABA91089 derived from expressed sequence tags (ESTs; ABA91056-CC ABA91089) derived from Physcomitrella patens cDNA libraries. The PKSRPS CC of the invention comprise protein kinase-6 (PK-6), protein kinase-7 (CFK-7), protein kinase-8 (PK-8), protein kinase-7 (CFK-7), casein kinase-6 (PK-8), protein kinase-7 (CFK-7), protein kinase-7 (CFK-7), protein kinase-7 (CFK-7), casein kinase-7 (CFK-7), protein kinase-7 (CFK-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New protein, useful for increasing tolerance to environmental comprises a Protein Kinase Stress-Related Protein selected fi Protein kinases, Casein kinase homologs, MAP kinases or Calci
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Sequence 683 BP; 172 A; 188 C; 163 G; 158 T; 2 other;

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                                                                               cggagaggccttatcgccgacggcaactgccaaagacgagattactcagatgatactaaa
aagagcgcggaggcggcgtaagtttgcgtggaagccggttttgcagagcatctccgagat
                                                                      cggagaggccttatcgccgacggcaactgccgaagacgagattactcagatgatactaaa
                                                                                                                                                                                         24.8%;
96.6%;
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pri misc_difference 3642  Fil misc_difference 3657  Fil misc_difference 3657  Fil misc_difference 3659  Fil misc_difference 3659  Fil misc_difference 3661  Fil misc_difference 3768  Fil misc_differenc	misc_difference 3641 /*tag= g /note= "this nucleotide is represented as a *		misc_difference	"this nucleotide is represen 'note" "this nucleotide is represen specification, and is inclusive base numbering given in the misc_difference 3631	_difference 3615 base numbering given in the specification, and is included base numbering given in the specification and is included base numbering given in the specification.	/note "this nucleotide is represented as a * in the specification, and is included to maintain misc_difference 3610 /*tag- b /note "this nucleotide is represented as a * in the specification"	Stealth virus.  Key misc_difference 3605	OF OB-SEP-1999 (first entry)  XX  DE Stealth virus nucleic acid clone, SEQ ID NO: 24.  XX  XX  XX  XX  XX	3 2/c x84332 standard; [ x84332;	Db 550 agggcaacgcgaaatctcttttatatggcgtagtttgtgtctccgactggactcctatct 609  Qy 1462 attcccccatcgagataactgcattcgttggataaatttctcccaacatt 1510	430 1346 490 1405	
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"this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  /*tag= aj /note= "this nucleotide is represented as a * in the specification and is included to maintain the	specification, base numbering  c_difference 3841  /*tag= ah /note= "this nucleotide specification, base numbering base numbering"	is represented as a * in the ind is included to maintain it in the specification in the specification in the specification is represented as a * in the is repres		ac  "this nucleotide is represented as a * in specification, and is included to maintai base numbering given in the specification ad	<pre>/*tag= aa /note= "this nucleotide is represent /note= "this nucleotide is represent specification, and is includ 8812  3812 /*tag= ab /note= "this nucleotide is represent specification, and is included."</pre>	misc_difference 3799  /*tag= z /note= "this nucleotide is represented as a * in the specification"  /*tag= z /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  misc_difference 3800		/*tag= v /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"  /*tag= w /note= "this nucleotide is represented as a * in the specification, and is included to maintain the base numbering given in the specification"
Oy 1704 ggattttcttgagcgcagatcttgcttccgcagtttgttt	Db 2193 GSHAGNRNSSYKGNGSDABKGDSNAYHNTDAACNHNSYYGSGNSHGTNKTSWDSNGSD 2136	2373 GNSHAYSNDASKTYDATYBSNHNTSTGSDANNGDAWHHBYSKTNTKNCBKGSYBKGDYBK  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacg  1524 ctcaagcagctcctcaatggccagtaatatgttacgacattgtgcacaactccaattacgacattgcacaactccaattacgacattacg		2613 1284 2553	1107 gaagagggggt	990 gagaggcctta : :  ::  2853 DADGKADCYDA 1050 gtgccgcaagg :: ::  2793 YBDATASDANA	Similari 9; Cons ttcgactt: :   :: WSNGKTYK	_difference _difference

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                                               The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
Sequence 5845 BP; 1294 A; 83 C; 1502 G; 2966 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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01-SEP-2000;
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2000DE-1043826
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                                            The invention relates to novel genes (ABA11004-ABA21534) and proteins CC (ABB14678-ABB18001) useful for preventing, treating or ameliorating CC medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC and ovarian cancer and other cancers of the adrenal gland, bone, bone CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital: CC (b) immune discrders e.g. Addison's disease, allergies, autoimmune CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative CC (d) wound healing; (e) cardiovascular discrders such as myocardial ischaemias; CC (d) wound bealing; (e) neurological diseases e.g. cerebral anoxia and CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal CC and parasitic infections.

CC Note: The sequence data for this patent did not form part of the CC printed specification, but was obtained in electronic format directly CC from WIPO at ftp.wipo.int/pub/published_pct_sequencess.
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The patent discloses a method for identifying genes that enhance levels of disease resistance if expressed in susceptible plants. The method is useful for isolating disease resistance genes (R gene) in plants. These genes confer non-host disease resistance to plants by responding to avirulence genes in plant pathogens. The R-genes identified trigger a hypersensitive response (HR) in tobacco that is dependent on the presence of the Phytophthora infestans elicitor INF1. The genes are useful for generating pathogen-resistant transgenic plants. They can be used to control viral, fungal, bacterial or nematodal pathogens, e.g. Phytophthora, Erisyphe and Puccinia. The present sequence is the
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45.7%;
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pathogen; fungal pathogen;
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                                                                       Sequence 3612 BP; 1042 A; 624 C; 911 G; 1035 T; 0 other;
                                                                                                             Nhrl gene which can activate a signal transduction pathway leading to induction of HR based on recognition of P. infestans elicitor, INF1 gene contains two zinc-finger like domains and a bromo domain, indicatibat Nhrl might be a transcription regulator or a signalling protein.
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11-JUL-2000;
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DB; ABB61757.
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2000US-0614150
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capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16180-ABL16175) and the encoded proteins

Claim 1; SEQ ID NO 12062; 21pp + Sequence Listing; English

invention relates to an isolated nucleic acid detection reagent

invention

ST

and

interactions

isolated nucleic acid es from Drosophila and

detection reagent for detecting for elucidating cell signalling

1000 and c

cell-cell

(ABB57737-ABB72072).
The sequence data for this patent did not form part of the prospecification, but was obtained in electronic format directly

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Sequence 7201 BP; 1933 A; 1731 C; 1808 G; 1729 at ftp.wipo.int/pub/published\_pct\_sequences.

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                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABLIG175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental pharmaceutical; gene; ss.
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P-PSDB; ABB66131.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 25184; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions
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                                                                                                                                                  The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                              Sequence
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11213 CATTGTTTCGCTGGCTGCATTCGCGAATTTCGGTGTATTTTTACGCATGATAA 11158

aattgaagcgcgtgaagcttcatctgtgatttttggaggttgtttttgactgatgagaa 179

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RESULT 9
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pharmaceutical; gene; ss.
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                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
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                                                                                                       Sequence 14458 BP;
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                        64
                                                                                                                              a sequence data for this patent did not form part of the printed scification, but was obtained in electronic format directly from ftp.wipo.int/pub/published_pct_sequences.
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DB; ABB66117.
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             agtcagcgagcaggctgagagttcggcagcgaagttacactcgacctggctgaaatttgg 123
JC,
                                               l Similarity 56.065; Conservative
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2000US-0614150.
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                                                                                                           3106 G;
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                                                                                                                                                          1934 talgacottotoatotattttogggotttgtttogagottoatgtacoatogactagogto 1993
                                                                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterioscierosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                       2054 atttgtacagtagcttgg 2071
                                                                                              877
                                                                                                                                                                                                                                                                        Sequence 8178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                       937
                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A,
                                                                                                                                                 817
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01-SEP-2000; 2000DE-1043826.
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                                    tttttagtttgtgttgg
                                                                                   atttttgtagagttttaaaggtatgtatatttagtatggtttgtttaatgatagttgga 936
                                                                                                       actttgactgcggtgataatcgtttgtcaatttagtggagctttgtagatgatagatgcc 2053
                                                                                                                                          taagtatttttacgtgttttaattttaaaattagtttttaattatttttgtatagcgtt 876
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 60;
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                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                       B₽;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rheumatoid arthritis; psoriasis;
                                                                                                                                                                                                               1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      associated gene SEQ ID
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Pred. No.
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bowel disease;
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abnormal
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Human
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COT Infe
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PPT Prepr
PT Prepr
PT Prepr
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PPT A (HUD)
PA 
                                               The polynucleotide sequences given in AAF33213 to AAF33261 encode the CC human secreted proteins given in AAB64930. AAB64931 to AAB64991 represent human secreted polypeptide sequences and proteins CC homologous to them, which are given in the exemplification of the present CC invention. Human secreted proteins have activities based on the tissues CC and cells the genes are expressed in. Examples of activities include: CC antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; CC vascular; antionvulsant; notropic; antialzheimers; CC vascular; anticonvulsant; notropic; antialzheimers; CC antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can be used in the prevention, diagnosis and treatment of diseases associated CC with inappropriate polypeptide expression. Disorders that may be prevented, diagnosed and/or treated by the above methods include immune CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and CC human immuno-deficiency virus (HIV) infections), hyperproliferative CC (e.g. Scimitar syndrome, Chaga's cardiomypathy and coronary CC (e.g. Scimitar syndrome, Chaga's cardiomypathy and coronary CC (e.g. Huntington's chorea, Alzheimer's disease), cardiovascular diseases (e.g. corneal graft coronary corona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnerary; antialzheimers; antiparkinsonian; antimicrobial; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV; infection; hyperproliferative disorder; cancer; Gaucher's disease; wound healing; cardiovascular disease; Scimitar syndrome; Chaga's cardiomyopathy; coronary arteriosclerosis; anglogenic disorder; diabetic retinopathy; corneal graft neovascularisation; neurological disorder; regeneration; Huntington's chorea; Alzheimer's disease; Parkinson's disease; infectious disease; chemotaxis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 49 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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Best Local Similarity
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           The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemio; cytostatic; nootropio; neuroprotective; anti-HIV; anticonvulsant; phthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
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                                                                                                                                                             cytosine
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                                                                                                                                                             methylation
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961.
                                                                                                                                   German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                           gene, us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2354;
                                                                                            The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                        usetul
                                                                                                          associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
       The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albheimer's disease, Alb, epilepsy, neurofibromatosis,
                                                                                                                                                                                                                                                                                                                                                                                        antiarteriosclerotic; antianzemic; cytostatic; nootropic; neuroprotective; anti-HTV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antirheumatic; ancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1066
                                                                                                                                                                                                                                           30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16994
                                                                                              Claim
                                                                                                                    cytosine
                                                                                                                             Nucleic acid comprising for diagnosis and treatm
                                                                                                                                                                                              01ek
                                                                                                                                                                                                                                                                                02-JUL-2001;
                                                                                                                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                                                                                                                WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL34445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL34445 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          886
                                                                                                                                                                                                                     (EPIG-)
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gttgtttgactgatgagaagaggtctctgagctgagaatgtttgcaatttaggggcacca
                                                                                                                                                                     2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccggtttgttggagtcccttgccacttattacaattgttggtttacaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attttgttttttattttatatttttagtttatacgattatatgagatttacggggagtt 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cactcgacctggctgaaatttggaattgaagcgcgtgaagcttcatctgtgatttttggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tttttttgttcggtgttggagtttgaagtttttagggtaggaggtcgggaagagaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ttgatttgtgaggcttcgtattgagtcagcgagcaggctgagagttcggcagcgaagtta 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107;
                                                                                              ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immune
                                                                                                                                                                                                                     EPIGENOMICS AG
                                                                                              SEQ ID NO 2418;
                                                                                                                    methylation
                                                                                                                                                                                            Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                           2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                rising fragment of chemically modified treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4165 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8486
                                                                                           32pp +
                                                                                                                                                                                             Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33.8;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                            Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2418.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 16994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
                                                                                                                                gene, use
abnormal
                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                               useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  220
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rheumatoid arthritis, psoriasis

and inflammatory/ulcerative bowel

diseases

The

present sequence is a gene of the invention

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RESULT 14
AAA10595/c
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                                                                                   Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                        This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
   6075
                                            6135
                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1707 ttttcttgagcgcagatcttgcttccgcagttttgtttcataacgttttggttcgtagggg 1766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5061 tttgtgatttcggagatcgttttttagtgacgagagcgggggtcggggcgttgtttcggt 5120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1647 tttgtgctttgggtatcccgttgtgacgagatgtcatgtcgcaccgtgcctatcagtggga 1706
                                                                                                                                      Sequence 6741
                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cellulose synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                 JP2000060568-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Vigna angularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene encoding a subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA10595 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                   26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                        26-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                            29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA10595;
                                                                                                                                                                                                                                                                                                                   (MIZU/) MIZUNO
(OJIP ) OJI PAF
                                                                78
                                                                                                                                                                                                                                                    gene encoding a cellulose synthetic equipment -
              CSRAKYSNCCDCYTNCSRCNSTCCYTCYSSRSRNCTTSRRCTBYRAYACSRSTSTDSRSR 6076
                                                            ctgagagttcggcagcgaagttacactcgacctggctgaaatttggaattgaagcgcgtg 137
RCNSTTTCTBTTCYTTTTSTSTTTNSTCDNSTTBDRCDSRGSRYSSRRCSTRCSTCYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-342371/30
                                                                                                                                                                                                                                  2
                                                                                  Similarity 17.6
78; Conservative
                                                                                                                                                                                                                                                                                     AAY85180
                                                                                                                                                                                                                                 Page 22-31; 32pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8486 BP;
                                                                                                                                                                                                                                                                                                                    PAPER CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                     BP; 1712 A;
                                                                                                                                                                                                                                                                                                                                                   98JP-0239998
                                                                                                                                                                                                                                                                                                                                                                        98JP-0239998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1852 A; 263 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.5%;
                                                                                            1.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         cellulose production; increase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6741
                                                                                   154;
                                                                                                                                      870 C; 1468 G; 1374 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellulose synthase
                                                                                            Score 33.4;
Pred. No. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 15;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.6;
Pred. No. 15;
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2416 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3955 T;
                                                                                                      DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DΒ
                                                                                   210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
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                                                                                                                                      1317 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                     for the body
                                                                                                      Length 6741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8486;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        yield;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds
                                                                                                                                                                                                                                                                improvement
                                                                                  2;
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
 6016
                     197
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RESULT 1
ABLJ33078
AD ABLJ3
AC ABLJ3
AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosts; anae acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6015
                                                                                                                                                                                                                                  cytosine methylation
                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL33078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL33078 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttggtttacaagctcgacgagtttcaatcgaacgtagagttttagtcgggtcgaggat 315-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system disease; cytosine methylation; antiasthmatic;
teriosclerotic; antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001WO-EP07537
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n abnormal
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The present invention provides a number of human immune system associating genes which are modified by the methylation of Cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and

associated

macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid

AIDS,

epilepsy,

neurofibromatosis

leukaemia,

Alzheimer's disease,

Claim 1; SEQ ID NO 1051; 32pp + Sequence Listing; German.

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CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.

XX
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 134 C; 2005 G; 4046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 105 A; 1046 T; 0 other;
SQ Sequence 8375 BP; 2190 A; 1046 T; 0 other;
SQ Sequence 83.4; 1046 T; 10
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Search completed: September 15, 2002, 23:46:06 Job time: 5230 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                No.
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Issued_Patents_NA:*

| Cgn2_6/ptodata/2/ina/5A_COMB.seq:*
| Cgn2_6/ptodata/2/ina/5B_COMB.seq:*
| Cgn2_6/ptodata/2/ina/5B_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6A_COMB.seq:*
| Cgn2_6/ptodata/2/ina/6B_COMB.seq:*
| Cgn2_6/ptodata/2/ina/backfiles1.seq:*
| Cgn2_6/ptodata/2/ina/backfiles1.seq:*
                                                                                                                                                                                                                                                                                                                                                Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-828-313-22
2177
1 atcccgggcttgtattggct.....gcagatattgccgttaacgc 2177
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1 US-08-232-463-14
2 US-08-278-989-11
4 US-09-272-796-11
4 US-09-103-840A-2
4 US-09-103-840A-1
3 US-08-963-1686-4
3 US-09-978-294-20
1 US-08-245-294-7
1 US-08-474-499-7
1 US-08-295-06211-7
5 PCT-US95-06211-7
5 PCT-US95-06211-7
1 US-08-26660-754-1
2 US-08-660-754-1
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5 PCT-US95-02520-1
1 US-08-96-364-2
2 US-08-96-364-2
3 US-08-96-384-2
3 US-08-96-384-2
3 US-08-9138-024-20
3 US-09-138-024-21
3 US-09-138-024-21
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                                                                                                                                                                                                                                                                      Sequence 14, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 2, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 20, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 1, Appli
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Sequence 21, Appli
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Sequence 11, Appli
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US-08-232-463-14
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29.6	29.6	29.6	29.8	29.8	29.8	29.8	29.8	29.8	29.8	30	30	30	30	30	30	30	30.4
1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4
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Sequence 5, Appl1	Sequence I, Appli	Sequence 3, Appli	, L	Sequence 1/, Appr	,	, ,	,	,	ט נ			ب د	,	4.		, 2	

ALIGNMENTS

; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHELFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS ; IMMEDIATE SOURCE: ; CLONE: pTZgpt-F1s US-08-232-463-14 APPLICATION UMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US/07/935,313
FILING DATE: US/07/935,313
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
APPLICATION UMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 30,472/114 IMM
REFERENCE/DOCKET NUMBER: 30,472/114 IMM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)83-4109
TELEPHONE: (703)83-4109 TELEFAX: (703)683-4109
TELEFAX: (899149
TINFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati NUMBER OF SEQUENCES: 5: CORRESPONDENCE ADDRESS: STREET: 1800 Dia CITY: Alexandria STATE: VA COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear COUNTRY: ADDRESSEE: Application US/08232463 E: Foley & Lardner 1800 Diagonal Road, USA 30472/114 IMMU Suite 500 #1.25

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Best Local :
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                             ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOSTWARE: FestSEO for Wind
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                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals,
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Goli, Surya K. APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1582 cgtagcgttattctgtaacccacgttcatcgaggtatcaaggaatggcgcagtaagcact 1641
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                                                TELEFAX:
                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl G.
                                                415-845-4166
                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                          SYSTEM: DOS
FastSEQ for Windows Version
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                  11:
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Pred. No. 0.0026
                                                                                               PF-0321
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09272796 Patent No. 6207148 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1935 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1489 ttggataaatttctccaacattttttgctcttcatcctcaagcagctcctcaatggccagt 1548
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LIBRARY: SYNORATO4
CLONE: 705365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1473 TCTTGGTTATGGGTGAATG 1455
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                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Corley, Neil C
APPLICANT: Guegler, Karl (
APPLICANT: Lal, Preeti
APPLICANT: Goll, Surya K.
APPLICANT: Shah, Purvi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES
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                                                                                                                    REFERENCE/DOCKET NUMBER: PF
                                                                        TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3174 POI
CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: UZIP: 94304
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72; Conserv
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Guegler, Karl G.
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                                                                                                                                                                                                                  08/878,989
                                                                                                                              PF-0321 US
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RESULY 5
US-09-103-840A-1/c
S-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
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; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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; Sequence 2, Application US/09103840A

; Patent No. 6294338
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; CLONE: 705365
US-09-272-796-11
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24356-2007.00
CURRENT APPLICATION NUMBER: U5/09/103,840A
CURRENT APPLICATION NUMBER: U5/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
SOFTWARE: Patentin Ver. 2.1
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Best Local Similarity 51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                            817 agtaacgatgcagcttgaatccatacgaaacgagggcccagagcctcacctcgctgg 876
                                                                                                                                                                                                                                          937 acttcctagaa 947
                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
mes 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 54;
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Sequence 4, Application US/08963168C
Patent No. 6127166
GENERAL INFORMATION:
APPLICANT: Bayley, Hagan
APPLICANT: Cao, Quiping
APPLICANT: Wang, Yunjaun
TITLE OF INVENTION: MOLLUSCAN LIGAMENT POLYPEPTIDES
TITLE OF INVENTION: AND GENES ENCODING THEM
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
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; ORGANISM: Mycobacterium tuberculosis; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
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                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOTTWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA: MAPPLICATION UNMBER: US/08/963,168C
FILING DATE: 03-NOV-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, Peter J.
REGISTRATION UNMBER: 32,983
REGISTRATION UNMBER: 07917/059001
TELEPHONE: 617/542-8906
TELEPHONE: 617/542-8906
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Best Local Similarity 52.7%;
Matches 69; Conservative
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 4411529
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                           TELLEFAX: 01.,
TELLEFAX: 200154
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STATE: MA

 Mismatches

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Pred. No. 54;
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; LENGTH: 458
; TYPE: PRT
; ORGANISM: Human
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CURRENT FILING DATE: 1998-08-26
NUMBER OF SEO ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 3.0
SEO ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09141000
Patent No. 6054295
GENERAL INFORMATION:
APPLICANT: Chen, Fang
APPLICANT: Chen, Fang
TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NUCLEAR
TITLE OF INVENTION: RECEPTOR PROTEINS
FILE REFERENCE: 19999Y
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Best Local S
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Best Local Similarity
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                       1659 tatcccgttgtgacgagatgtcatgtcgcaccgtgcctatcagtgggattttcttgagcg 1718
                                                                                                                                                                                                                                           1479 actgcattcgttggataaatttctccaacatttttgctcttcatcctcaagcagctcctc 1538
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                                                                                              1599 acccacgttcatcgaggtatcaaggaatggcgcagtaagcactgctactttgtgctttgg 1658
                                                                                                                                                                       1539 aatggccagtaatatgttacgacattgtgcacaactccaattacgtagcgttattctgta 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1
                                                                                                                                                                                                                                                                                   442 C...M.NR.D.BTMASA.Y....AK.KMCTYY.H.KD.CT.RH..T.D.BH..M.BT.BH. 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 GCCGCCTCCCATTCCGCCGAAACCGGCATTTCCGCCTCCCATTCCTCCGAAACCTCCCAT 280
                                                                                                                                                                                                        382 .DKSHSNT.T.TM.AB...M..MKSMRMMB....TNN.H..CT.MS.H.HK.RHHTRB.. 323
                                                                                                                                   322 H..S.SYRBBC....KWTS...SK.HT.S.AS.C..DMTWC..BB..YHT.HG.AA.TM 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 GCCTTTACCTCCGCCCATTCCGCCCATACCGCCGAATCCGCCTGCGTTCATTCCGC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ACCGAATCCGCCTGGACCTCCACCCATACCACCTCCGAAGCCGCCTATTCCGCCGAATCC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ACCACTGCCCATTCCTCCGAATCCACCTTTCGCCGCCATTCCGCCGAAACCTCCCCATTCC 220
                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 396 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                            .HSH.BA.H.KTR.M...TB..DSB.MNR.MMT..B...N.R.SN.TH.YYMRM.YCCYB 203
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8.7%; Pred. No. 1.6;
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Pred. No. 1.5;
0; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               DB 3;
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US-09-078-294-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08245294 Patent No. 5644047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09078294 Patent No. 6265211
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CURRENT FILING DATE: 1998-05-13
NUMBER OF SEQ ID NOS: 29
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APPLICANT: Du Sart, Desiree
APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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APPLICANT: Regnery,
TITLE OF INVENTION: INTITLE OF INVENTION: INTIT
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                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   472 gtacaattttttactcttcgaagacagaaaatttgctgacattg 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 127 PO
CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
FILING DATE:
                                          APPLICATION NUMBER: US/08/245,294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YH.YBC.M.KCBM.GMK.YGT.GSMYYYMA..G.NAT.GSR..NC..AYM..TMGT.GST 143
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l Similarity 55.8%;
58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEEDLE & ROSENBERG, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Burt E.
Russell L.
METHODS AND COMPOSITIONS
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ROCHALIMAEA HENSELAE AND ROCHALIMAEA QUINTANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFECTION
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0; Mismatches
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; LOCATION:
US-08-245-294-7
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US-08-474-499-7/c
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TELEPAX: 404/588-9880
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
FRIGHH: 1791 base pairs
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Best Local Similarity 50.0%;
Matches 76; Conservative (
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                                                    CLASSIFICATION: 536
PRIOR APPLICATION NAME: US 08/245,294
PFLICATION NUMBER: US 08/245,294
FILING DATE: 18-MAY-1994
ATTORNEY/AGRET INFORMATION:
NAME: Spratt, Gwendolyn D.
                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION UNMER: US/08/474,499
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1519 tcatcctcaagctgctcctcaatggccagtaatatgttacgacattgtgcacaactccaa 1578
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ATTORNEY/AGENT INFORMATION:
NAME: Spratt, Gwendolyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Regnery,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CITY: Atlanta
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REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 14
                                   NAME: Spratt, Gwendo
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                 NAME: Spratt, Gwendolyn D. REGISTRATION NUMBER: 36,016 REFERENCE/DOCKET NUMBER: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCGTCTTCAGGCATCGAATCAAGTTTAACCTTAATATTCTCTTTTACCAGATTTCCAA 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                     30303
                                                                                                                                                                                                                                                                                                                                                                      Georgia
                                                                                                                                                                                                                                                                                                                                                                                                              127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anderson, Burt E.
Regnery, Russell L.
VENTION: METHODS AND COMPOSITIONS FOR
VENTION: DIAGNOSING ROCHALIMAEA HENSELAE
DIAGNOSING ROCHALIMAEA INFECTION
EQUENCES: 10
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141..1649
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INFORMATION
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Pred. No. 7.8;
0; Mismatches
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                 1414.612
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; LOCATION:
US-08-474-499-7
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Best Local S
Matches 76
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INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 1791 base pairs
TYPE: nucleic acid
                                                                                   TELEFAX: (404) 688-9880 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS:
STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/307,279A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, Burt E.
APPLICANT: Regnery, Russell L
TITLE OF INVENTION: and Methods and Compositions for Diagnosing Rochalimaea
TITLE OF INVENTION: Henselae and Rochalimaea Quintana Infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1330
                                                                                                                                       REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 688-0770
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MEDIUM TYPE: Floppy disk
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                                             TYPE: nucleic acid
                                                                                                                                                                                           NAME: Spratt, Gwendolyn D. REGISTRATION NUMBER: 36,016
                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Atlanta
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76; Conserv
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                                                                     1791 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-307-279A-7
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; LOCATION:
PCT-US95-06211-7
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PCT-US95-06211-7/c
; Sequence 7, Application PC/TUS9506211
; GENERAL INFORMATION:
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Best Local Similarity
""+ches 76; Conserve
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1791 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
           Query Match
Best Local S
Matches 76
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PRIOR APPLICATION NUMBER: PRICE DATE: 18 MAY 19
PRICE CLASSIFICATION:
CLASSIFICATION: PRICE DATE: 19
PRICE DATE:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: Atlanta
CITY: Atlanta
CTATE: Georgia
USA
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NAME: Spratt, Gwendolyn D.
REGISTRATION NUMBER: 36,016
REFERENCE/DOCKET NUMBER: 141
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: NEEDLE & ROSENBERG, P.C.
STREET: 127 Peachtree Street, Suite 1200
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ZIP: 30303
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       ch 1.4%;
l Similarity 50.0%;
76; Conservative
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141..1649
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141..1652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
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Score 30.4; D
Pred. No. 7.8;
0; Mismatches
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                                                              DB 5;
   76; Indels
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NAME: KAGAN, SATAh A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELEPOMUNICATION INFORMATION:
TELEPHONE: 202.508.910
TELEFAX: 202.508.929
TELEEX: 197430 BMMB UT
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                    Matches
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APPLICANT:
APPLICANT:
                    2124 gtattatttaaacctatatgaagtgaacggctgtgcagatattg 2167
                                                                                  2064 tagcttggatgctgttttacaagatagcggcagctagaagccttaaacctttagctaccat 2123
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRINT APPLICATION DATA: APPLICATION NUMBER: US/08/204,679 FILING DATE: 02-MAR-1994 CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1270 ACTCCTAAGGTTACTGTTTCTCCTGGGCTCAT 1239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1390 TCCAATGTTTCATCTGAATTACCGTGCTCATTTGAATATTTTGAGCCATCCTTCATATTT
665 GTACAATTTTTTACTCTTCGAAGACAGAAAATTTGCTGACATTG 708
                                                               605 TATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCCAA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: D.C.
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1001 G Street, N.W.
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                                                                                                                                 1.4%;
ilarity 55.8%;
Conservative
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VENTION: In Vitro Transposition of Artificial
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                                                                                                                               Score 30.4; D
Pred. No. 14;
0; Mismatches
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                                                                                                                                                               DB 1;
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TOPOLOGY: Circular

MOLECULE TYPE: DNA (9e

HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
US-08-660-754-1
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          Sequence 1, Application US/08796364
Patent No. 5968785
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR DEPLICATION DATA:
PRIOR DATE: US 08/204
FILING DATE: O2 MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION UMMBER: 32,141
REFERENCE/DOCKET NUMBER: 0110
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMUNICATION:
TELECOMUNICATION 202.508.9100
TELEEAX: 197430 BBMB UT
INFORMATION FOR SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                    Query Match 1.4%;
Best Local Similarity 55.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08660754 Patent No. 5843772
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APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
                                                                                                                                                                            2124 gtattatttaaacctatatgaagtgaacggctgtgcagatattg 2167
                                                                                                                                                                                                                                                          2064 tagcttggatgctgtttacaagatagcggcagctagaagccttaaacctttagctaccat 2123
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CURRENT APPLICATION DATA:
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APPLICANT:
                                                                                                                                                         665 GTACAATTTTTTACTCTTCGAAGACAGAAAATTTGCTGACATTG
                                                                                                                                                                                                                                605 TATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCTAAAGGCATTATCCGCCAA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPUTER READMADLE. Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPTUBARPE: PatentIn Release #1.0, Version #1.25
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                   58; Conservative
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1001 G Street, N.W.
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Search completed: September 16, 2002, 01:17:18 Job time: 12612 sec
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; CLONE: pat-1
US-08-796-364-1
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Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
TELEX: 197430 BBMB UT
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/204,675
APPLICATION UMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT IMFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION UMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.4550
                                                                                                                  2124 gtattatttaaacctatatgaagtgaacggctgtgcagatattg 2167
                                                                                                                                                                                      2064 tagcttggatgctgtttacaagatagcggcagctagaagccttaaaacctttagctaccat 2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,364
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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                                                                                                                                                           605 TATCTTGACTGATTTTTCCATGGAGGGCACAGTTAAGCCGCCTAAAGGCATTATCCGCCAA 664
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
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                                                                                      GTACAATTTTTTACTCTTCGAAGACAGAAAATTTGCTGACATTG 708
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1001 G Street, N.W.
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Braiterman, I
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Result
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Maximum DB
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
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Perfect score:
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      290.8
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Match
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2177
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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em_estov:*
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    1101
553
671
577
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940
1001
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2 CNS011PE
2 CNS011PE
2 CNS011PO
AW62536
3 CNS0100
AW62536
4 W62536
AW930530
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             CNS03F69
AI775253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Search time 1744.24 Seconds (without alignments) 16845.658 Million cell updates/sec
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           BJ179058 BJ179058
BJ174514 BJ174514
BJ174524 BJ174924
AW739415 gb41f06 y
AL100556 Drosophil
AG029463 Pan trogl
AW625386 EST319209
AW930530 EST340987
AG155394 Pan trogl
BG357216 HVSME3000
BF623571 HVSME3000
AL073444 Drosophil
BB7304 RPCIII - 28H1
AL241290 Tetraodon
AI775253 EST256353
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BM407305 EST581632
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	35.2			35.4	35.4	35.6	35.6	35.6	35.8	35.8	35.8	36	36	36	36.2	36.2	36.2	36.2	36.4	36.4	36.4	36.6	36.6	36.6	36.8	36.8	36.8
1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.6	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7
519	518	506	778	711	415	790	789	286	836	359	353 3	469	432	418	1101	507	449	438	1101	1067	307	952	611	497	1028	872	501
9	10	10	9	12	12	12	12	9	10	10	9	10	9	12	12	12	12	10	12	10	9	9	9	12	12	10	10
AI164309	BE805900	N95351	AV384757	AZ319283	AZ223450	вн250073	BH450439	BB415825	BF623428	н62450	AI362949	BG726049	AI410421	AQ340838	CNS0129R	AZ498987	AZ498999	BM136567	CNS000D1	BF529057	BB104250	BE037533	BE111776	AQ772166	CNS00JPV	BF159188	BG405233
AI164309 A059P10U	BE805900 ss62q10.v	N	Þ				BH450439 BOGOT14TF		BF623428 HVSMEa000	H62450 vr79f08.r1	AI362949 gv87f05.x		EST238714		AL101289 Drosophil					7	BB104250		UI-R-BJ1-				BG405233 sac49h03.

ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM FEATURES RESULT BJ179058 COMMENT REFERENCE DEFINITION LOCUS TITLE JOURNAL AUTHORS Email: tshini@genes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo
excised from a modified IPS phage vector (Mo bi Tec, Germany). XhoI
digested-5' end of cDNA is ligated to SalI site of the vector, and
the BamHI digested-3' end including poly-A tail is ligated to BamHI
site of the vector. cDNA instert could be amplified with
conventional T7 and T3 primers. This normarized full-length cDNA
library was generated basically according to the method described
in Genome Research ID, 1617-1630 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on
the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13
days under the continuous light. Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan 1 (bases 1 to 294)
Fujita,T., Shin-i,T., Seki,M., Kamiya,A., Uchiyama,I., Nishiyama,T.,
Carninci,P., Hayashizaki,Y., Shinozaki,K., Kohara,Y. and Hasebe BJ179058 mRNA lin BJ179058 normalized full length cDNA library, caulonemata and malformed buds Physcomitrella cDNA clone pphb24a07 5', mRNA sequence. BJ179058 BJ179058.1 GI:18347012 plants genome Unpublished (2002) Physoomitrella patens subsp. patens.

Physoomitrella patens subsp. patens

Physoomitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;

Bryopsida; Funaridae; Funariales; Funariaceae; Physoomitrella. Tel: 81-559-81-6856 Fax: 81-559-81-6855 Contact: Tadasu Shin-i Comparison of the moss Physcomitrella patens genome with flowering Location/Qualifiers
1. .294 linear chloronemata, patens subsp. patens EST 24-JAN-2002

source

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ACCESSION
VERSION
KEYWORDS
SOURCE
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Email: tshinlegenes.nig.ac.jp
A backbone of the vector is pBluescript II, that was in vivo excised from a modified IPS phage vector (Mo bi Tec, Germany). Xhol digested-5' end of cDNA is ligated to SalI site of the vector, and the BamHI digested-3' end including poly-A tail is ligated to BamHI site of the vector. cDNA instert could be amplified with conventional T7 and T3 primers. This normarized full-length cDNA library was generated basically according to the method described in Genome Research 10, 1617-1630 (2000), Carninci, P. et al.
Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13
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Physcomitrella patens subsp. patens.
Physcomitrella patens subsp. patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
I (bases 1 to 547)
Fulita T Streit Schila Kamiya A Hochiyama T Nichiyam
                                                                                                                                                                                                                                             Contact: Tadasu Shin-1
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
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BJ174514
BJ174514.1 GI:18342479
                                                                                                                                                                                                           Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Carninci,P., Hayashizaki,Y., Shinozaki,K.,
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/db_xref="taxon:145481"
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/clone=lib="normalized full length cDNA library,
/clonemata, caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonema
malformed buds"
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ella patens subsp.
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K., Kohara,Y.
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RESULT BJ174514

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                                                                                Physcomitrella patens subsp. patens.

physcomitrella patens subsp. patens

Endromitrella patens subsp. patens

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;

Euyopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.

1 (bases 1 to 605)

1 (bases 1 to 605)
                                       Fujita, T., Shin-i, T., Seki, M., Kamiya, A., Uch, Carninci, P., Hayashizaki, Y., Shinozaki, K.,
Comparison of the moss Physcomitrella
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chloronemata, caulonemata and malformed buds"
/tissue_type="mixture of chloronemata, caulonema
malformed buds"
malformed buds"
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                                            Uchiyama,I.,
K., Kohara,Y.
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                                              Nishiyama, T. and Hasebe
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Protonemata were blended by the POLYTRON, and then cultivated on the BCD medium containing 0.5um BA (benzylaminopurine) for 8 to 13 days under the continuous light.
               Ouatrano, R., Bashiardes, S., Cove, D., Cuming, A., Knight, C., Clifton, S., Marra, M., Hillier, L., Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Steptoe, M., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW739415 526 bp mRNA linear ES gb41f06.yl moss EST library PPN Physcomitrella patens PEP_SOURCE_ID:PPN161512 5', mRNA sequence.
                                                                                                                                                                                                                                Physcomitrella patens.
Physcomitrella patens
Physcomitrella patens
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
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/clone="pphb13n04"
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Pred. No. 3.9e-23;
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                                                                                                                                                                                                                                                                                                                                                                    62 AGCAGCTTCTCAAGAGAGTGATTGTTTGTCCAAGAGATTCTCTCCACC 109
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN06M20 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL100556
AL100556.1 GI:5612167
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Contact: Ralph Quatrano
Leeds/Wash U Moss EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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/lab_host="DH10B"
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/clone_lib="Moss EST library PPN
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/db_xref="taxon:3218"
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TGAAGGGTKTTTTAWGAAWAAKGWATTTGKTWTTTARAGGAAGATTTGTATTATTTTT 157
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                                                                                                                                                                                                                       acatcccatagaacatagtgcttcacttctgggttgttcaccactaggatcatatgacct 1941
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 855)
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/clone="BACNO6M20"
/note="end : SP6"
a 63 c 75 g
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                         434
                                                                                                                                                                                                                                                                                                                       208 tttaggggcaccaccggtttgttggagtcccttgccacttattacaattgttggt 262
                                                                                                                                                                                                                                                                                                                                                                                   494 TGTGATTCGGGCGCTGGTGTAAATTTGGAGAATGGTGGTGTGTGGGCTGGGCGGGTTGTTTG 435
                                                                                                                                                                                                                                                                                                      TTTAGGGTGGGAATTGATTTGGTGCAGGTCTGTTGGTCTTAGTTCAATTGTTGGT
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                                                                                                                       fly), ge
AL068607
                                                                                                                                                       CNS00TOO 1101 bp DNA linear GSS 03-JUN-1: Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR32D23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-c1.503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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311 c 100 g 208 t 5 others
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/clone="PTB-001I22.F"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Naron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be incremited Control of the library of the library and how to order individual BAC clones, the entire library.
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Lycopersicon esculentum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR32D23"
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                                                                                                                                                                                   cDNA clone
                                                                                                                            553 bp mnum., 5 d post-imbibition, Cornell ....
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                        Clemson University Genomics Institute Clemson University
                                                                                                                                  Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Generation of ESTs from tomato fruit tissue
                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum
Eukaryota; Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                         Contact: CUGI
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100 Jordan Hall, Clemson,
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Clemson University Genomics Institute
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/dev_stage="seedlings 5 days post-imbibition"
/dev_stage="seedlings 5 days post-imbibition"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="vector: pBlueScript SK(-); Site_1ecoR1; Site_2:
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="vector: pblueStript Site_1: EcoR1; Site_2: 
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/clone="cLEZ13E15"
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/cultivar="TA496"
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Local Similarity 52.9%;
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GI:16685072
AG155394.1 GI:16685072
GSS; GSS (genome survey sequence).
Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-019L05.TJ.
Pan troglodytes
Pan troglodytes
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5 prime sequence.
                                                                                                         Fujlyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Subhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                       of clone tracking errors. PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                             BAC
                                                                                                                                                                                                                                                                                                                                                                                                              Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/Nol; cLEF - Fruit were tagged at the 1cm stage and 
harvested 3-5 days prior to ripening. Fruit were cut in 
half to verify the seeds were indeed 'immature' and the 
seeds and locules were discarded prior to freezing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4081"
/clone="cLEE50G3"
/clone_lib="tomato fruit mature green, TAMU"
/clsue_type="fruit pericarp"
/dev_stage="mature green (3-5 days pre-ripening)"
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/cultivar="TA496"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
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Matches 99
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                                                                                                                                                                                                                                                   Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 513)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 20 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG367216 513 bp mRNA linear EST 22-OCT-2001
HVSMEi0011F10f Hordeum vulgare 20 DAP spike EST library HVcDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMEi0011F10f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare
                                                                                                                                                        Email: rwing@clemson.edu
Total hg bases = 368
Total hg bases = 368
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: Sequence stop: 506.
                                                                                                                                                                                                                                                                                                                                                                                        On Mar 8, 2001
                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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R.Site 2 : ECORI
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/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
, 99 c 88 g 189 t 1 others
                      /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSME10011F10f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pan troglodytes"
/db_xref="taxon:9598"
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/sex="male"
                                                                                                                                       Location/Qualifiers
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/clone_lib="Hordeum vulgare 20 DAP spike EST library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGCGGCGCAAGCGGCGAGCTCGGCGTCGGAGGGCGGCTCCCCGGCGGCGGCGGCGCT 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          agtgtcccgcaaaggagcagtcctccgccgaagaacgtctcaccacctcccccagcccgca 1345
                                                                                                                                                                         l (bases 1 to 940) Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF623571 940 bp mRNA linear EST 17-OCT-200
HVSWEA0002N05f Hordeum vulgare seedling shoot EST library
HVCDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0002N05f
                                                                  Contact: Wing RA
                                                                                                On Dec 18, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BF623571
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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University Genomics Institute University
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/tissue_type="20 DAP spike"
/lab_host="SOLR"
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                                                                                      this sequence version replaced gi:11887305
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Pred. No. 7;
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                                                                                                                                                                                                                                                                                                                                                                                                          CNS00HG7 1001 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR15A06 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL073444 1 GI:4953224 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: rwing@clemson.edu
Total hq bases = 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchor are resources for barley genomics. Barley Genetics Newsletter 31:39-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*

266 c 226 g 217 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genome.clemson.edu/projects/barley. To order
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HVcDNA0001 (Cold stress)"
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/lab_host="TJC121"
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/db_xref="taxon:4513"
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Pred. No. 11;
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nes 72; Conserv
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Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Drosophila.

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Homo Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 513)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.
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B87304.1 GI:2928436
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Golden, K.,
                                                                                         Homo sapiens
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR35A06"
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209 c 148 g
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Berry, K.,
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Other GSSs: RPCIII-28H13.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                             sequence.
AL241290
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Use of BAC End Sequences for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                     GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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freshwater pufferfish Unpublished
                                                                                           Roest-Crollius, H., Jaillon, O.,
                                                                                                           Tetraodontidae; Tetraodon.
1 (bases 1 to 1067)
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                                                          Weissenbach,J
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/clone="RPCI-11-28H13"
/clone_lib="RPCI-11"
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/db_xref="GDB:7510548"
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.iarc.ord/de/humaco/hac.end/search/hac.end/search
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNS03F69 1067 bp DNA linear GSS 17-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
021D17 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                              Charaterization and repeat analysis of the compact genome of the
                                                                                                   Bouneau, L., Billault, A., Quetier, F., Saurin, W.,
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
a 105 c 74 g 156 t
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Pred. No. 8.1;
Tetraodon nigroviridis
                                                                                                                                         Dasilva, C., Fizames, C.,
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Euteleostei; Neoteleostei
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                                                                                            504 TAGTTTGTGGTAAAGTTT 487
                                                                                                                                                                                                                                            Genoscope.

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

1. 1067
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
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/db_xref="taxon:99883"
/clone="021D17"
/clone_11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : C0BG021CB09LP1-end : T7"
/note="Genoscope sequence ID : C0BG021CB09LP1-end : T7"
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Copyright (c) 1993 - 2000 Comp
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Arabidops	AAG29282	21	734	٠	100	
	AAG29283	21	632		100	
Drosophila	ABB68041	22	611		100	
Mouse YNKl	AAY57448	21	382		100	
Drosophila	ABB61913	22	1540		101	
M. tuberculosis	AAY39026	20	679		101	
M. tuberculosis	AAY39169	20	679		101	
Mycobacterium tube	AAW64372	19	679		101	
M. tuberculosis	AAW81739	19	679		101	
Human cell	AAY44247	21	519		101	
Drosophila	ABB68471	22	795		101.5	
Drosophila	ABB58808	22	590		101.5	
Drosophila	ABB59466	22	1231		102	
Transcriptional	AAY72782	22	2973		103	
Protein used in ca	AAY70304	21	2973	٠	103	
Human APC	AAW76821	19	2973		103	
Adenomatous	AAR63507	15	2860	5.9	103	
Human APC	AAB23011	21	2843		103	
Human adenomatous	AAW38370	19	2843		103	
Human APC	AAW76144	19	2843		103	
Human APC	AAW76140	19	2843	•	103	
Human adenomatous	AAW35392	18	2843		103	
Adenomatous	AAW11922	16	2843		103	
Adenomatous	AAR58634	15	2843		103	
APC gene product	AAR26052	13	2843	5.9	103	
Adenomatous	AAR63508	15	2842		103	
Human androgen	AAB82946	22	2783	•	103	
AFP-1 (Ala	AAR23963	13	2783	5.9	103	

## ALIGNMENTS

## RESULT ABB700011 ID ABB7 XX ABB7 XX CABB7 XX CAB ABB70001 standard; Protein; 1381 23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-0614150 WO200171042-A2 Drosophila melanogaster. Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical. Drosophila melanogaster polypeptide SEQ ID NO 36795. 26-MAR-2002 (first entry) ABB70001; 23-MAR-2001; 2001WO-US09231. 27-SEP-2001. Venter JC, Adams M, (PEKE ) PE CORP NY. \_ Ŀi PWD, Myers Ą W

New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -  $\,$ 

WPI; 2001-656860/75. N-PSDB; ABL14104.

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                                    Modified-site
                                                                                                Region
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                                    /label= Protein-like_tandem_repeats
                                                                                                                                                                                                                 /label- Sig_peptide
35..158
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159..353
/label= N-glycosylation_site
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RESULT
AAB20062
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 Overlapping cDNA clones obtd. from a bovine brain cDNA library were combined (see AAT05627) to provide cDNA coding for bovine brevican (AAR85442). The brevican can be used to modulate axonal growth and to raise antibodies used in detection of gliosis.
Key
                        Arabidopsis thaliana
                                                Gene silencing; silencing
                                                                         Arabidopsis thaliana silencing gene-encoded protein.
                                                                                                   23-APR-2001
                                                                                                                            AAB20062;
                                                                                                                                                     AAB20062 standard; Protein; 2001 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 42-44; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalian brevican protein - directs/inhibits axonal growth, treatment of neuro-fibromatosis and in detection of gliosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shimonaka M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                            140 PEPHLAGDRPSKHLKLVFIRHCLRALRLPR-----ISIDLME-----SPLPNLS 183
                                                                                                                                                                                                                                        287
                                                                                                                                                                                                                                                               482 wpselssldpeaplptepvpeesltgasppvraalgpgvspppydepeaprpprvlgppt 541
                                                                                                                                                                                                                                                                                                                 425 aea--prtllefe-tqsivpplgsseeegkvleqeekyrgeeekeeeeeeeevedealwa
                                                                                                                                                                                                               542 ktlptpregnlaspppstlvgareieeetggpelsgaprgese 584
                                                                                                                                                                                                                                                                                         233 WKPVLQSISEMKPVMEFHTPMAYRDSGSPPKNA-----STPSLPGPKNISPPRQVSVPQ 286
                                                                                                                                                                                                                                                                                                                                         184 GEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFYLRRARRRK-----FA 232
                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                        RSSPPPKN---VSPPPQPAFVARTASKYSAASQQVQRNRGNAK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1995-351200/45.
DB; AAT05627.
                                                                                                                                                                                                                                                                                                                                                                  pashlasdale---aivtvtetleelklpqeavesesrgaiysipiiedggggsstpedp 424
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54; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   912 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94US-0219642.
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815..875
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/label= Central_region
649..684
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 116; DB 16; Length 912; 24.2%; Pred. No. 0.051; tive 26; Mismatches 101; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRP-like_region
                                                 gene;
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                                                   MOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamaguchi
                                                                                                                                                                                                                                                                                                                                                                                                                       42;
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                                                                                                             Query Match
Best Local S
Matches 82
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                                                                  1645
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                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                           Claim 1; Page 32-39; 48pp; English.
                                                                                                                                                                                                                                                                                                                                 Novel gene encoding a protein that controls particular silencing of plant genes -
                                                                                                                                                                                                                                                                                                                                                                                                     Habu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUN-2000; 2000WO-EP05761
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                       1701 --sagvtalv---
112 THGSQQSRKVF-DYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIR--HCLRA---L 165
                                             62
                                                                                        2 GLTPFSCVTVQGYVRVVYPDGHVENLSKSCSVHDLLLGNPDYYVCGSTPYTITNRMAAEE 61
                                                                 gnhpdtavniegldntsvaephisg-sdac---emeisepgpgverstfanlfheggveh 1700
                                                                                                                                                                                                                                                                                                                                                                               2001-137952/14
                                            VLEYGVTYFVCATPNAQPFLERQPKVVHRGSKIL-----PRFSKHGVHVRELRSP 111
                                                                                                                82;
                                                                                                                                                                                                                                                                                                                                                                                                                         NOVARTIS AG. NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                              Similarity 20.4
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                   AAA89353,
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                                                                                                                                                                                            regulating
                                                                                                                                                                       2001 AA;
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1219
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479..719
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858..8
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/note= "internal repeat region"
362..367
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1899..1
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                                                                                                                        6.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "predicted membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "nuclear localization motif"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "nuclear localization motif"
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family SWI2/SNF proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "nuclear localization motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "actin-binding domain"
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                     --psllnngteqiavqpvpqipfpvfndpflh--elekl 1743
                                                                                                                56;
                                                                                                             Score 105.5; 1
Pred. No. 1.5;
56; Mismatches
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                                                                                                                                     DВ
                                                                                                                128;
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                                                                                                                                      22;
                                                                                                                                                                                                                                                                                                                                             silencing,
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana silencing gene-encoded protein.
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Habu Y,
                 (NOVS ) NOVARTIS AG.
                                                                 21-JUN-2000;
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                                                                                                       WO200100801-A2
                                                                                                                                    Domain
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Mittelsten Scheid O,
                                                                                                                                                                                                                                                                                                                                                                                       thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                 2000WO-EP05761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -PPQPAFVARTASKYSAASQQVQRNRGNAKSL 328
                                              99GB-0014623
                                                                                                                                                                                           /note= "predicted membrane-spanning domain"
1219
                                                                                                                                                                                                                                                     /note=
832..8
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479..719
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1899..1941
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                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                          'note=
                                                                                                                                                                 'note=
                                                                                                                                                                                 'note= "Glu in ecotype Zurich"
                                                                                                                                                                                                                       note= "nuclear localization motif"
                                                                                                                                                                                                                                          note=
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                                                                                                                          "actin-binding domain"
                                                                                                                                                                                                                                                             "Met in ecotype Zurich"
                                                                                                                                                                                                                                                                                                            "ATP/GTP-binding motif"
                                                                                                                                                                                                                                                                               "region of homology to ATPase/helicase
family SWI2/SNF proteins"
                                                                                                                                                                                                                                                                                                                              "nuclear localization motif"
                                                                                                                                                                                                                                                                                                                                                  "internal repeat region"
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Amedeo P,
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                                                                                                                                            repeat region'
                                                                                                                                                               repeat region"
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Paszkowski
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2001WO-US01239

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Matches 82
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Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood related disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulating gene expression.
Note: the present sequence is not shown in the specification but is derived from the A. thaliana mutant silencer gene protein sequence given in AAB20062.
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                                                                                                                Novel human
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                                                                                                                                                                                     AAU22961;
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DB; AAA89385.
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82; Conservative
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                                                                                                                                                                                                                        standard;
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                                                                                                              enzyme polypeptide #47.
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                          Protein;
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Pred. No. 1.5;
56; Mismatches
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               14-AUG-2000
12-AUG-2000
22-AUG-2000
22-AUG-2000
22-AUG-2000
23-AUG-2000
23-AUG-2000
23-AUG-2000
01-SEP-2000
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07-JUL-2000;
07-JUL-2000;
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11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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04-FEB-2000;
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19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-2000;
17-MAR-2000;
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           2000US - 0180628
2000US - 0180628
2000US - 0180350
2000US - 0180350
2000US - 0198123
2000US - 0198123
2000US - 0211486
2000US - 02116880
2000US - 02116880
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2000US - 02118290
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2000US - 0224518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 60; Conserv
            Human extracellular matrix and cell adhesion molecule-7 (XMAD-7).
                                                    06-AUG-2001
                                                                                                                          AAE03643 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                         AAE03643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
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N-PSDB; AAS40831.
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21.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 105; DB 22;
; Pred. No. 0.29;
42; Mismatches 106;
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2000US-0246525. 2000US-0246526. 2000US-0246527.

2000US-0246478. 2000US-0246523. 2000US-0246524.

25-SEP-2000 26-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 29-SEP-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 03-OCT-2000 04-OCT-2000 05-OCT-2000 06-NOV-2000 08-NOV-2000 09-NOV-2000 09-NOV-2000 09-NOV-2000 09-NOV-2000 01-NOV-2000 01-NO

2000US-0241221 2000US-0241785

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2000US-0241808 2000US-0241809 2000US-0241826 2000US-0244617 2000US-0246474 2000US-0246475 2000US-0246477 2000US-0246477

17-NOV-2000
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01-DEC-2000
05-DEC-2000

2000US -0246528 2000US -0246532 2000US -0246610 2000US -0246611 2000US -0246611 2000US -0249207 2000US -0249210 2000US -0249211 2000US -0249211 2000US -0249211 2000US -0249211 2000US -0249213 2000US -0249214 2000US -0249216 2000US -0249216 2000US -0249216 2000US -0249216 2000US -0249216 2000US -0249216 2000US -0249244 2000US -0249244 2000US -024924 2000US -024926 2000US -024926 2000US -024926 2000US -024926 2000US -0251988 2000US -0251988 2000US -0251868 2000US -0251868 2000US -0251868 2000US -0251868 2000US -0251868 2000US -0251868 2000US -0251869 2000US -0251869

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CC or antagolist are used for treating a disease or condition associated converted as the approximate of the control of the co
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bacterial, fungal, parasitic, protozoal and helminthic infections and cell proliferative disorders such as actinic keratosis, arteriosclerosis and cancer including breast, bladder, bone marrow, brain and uterus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       effectiveness as an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAD08051.
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16-DEC-1999;
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                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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DNA encoding chicken C-ski proteins - used to produce transgenic animals having increased muscle growth, and to treat muscle degeneration or obesity
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                                                                                                                                               IRS-2; insulin receptor substrate-2; diabetes; therapy,
                                                                                                                                                                                                         16-AUG-1996
                                                                                                                                                                                                                                    AAR96994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
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                           /label= IH1
/note= "IRS-homology domain
190..366
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/note= "IRS-homology domain II"
                                                                                  Location/Qualifiers
                                                                                                                                    antibody; transgenic animal
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Mouse insulin receptor substrate-2, or IRS-2 (AAR96994), is substrate for the insulin receptor, interleukin-4 receptor interleukin-15 receptor, and can be phosphorylated by these
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                                    Disclosure;
                                                   New insulin receptor substrate polypeptide and corresp. nucleic - vectors, antibodies etc., useful for diagnosis, treatment and assessing risk of diabetes etc., also for drug screening
                                                                                       WPI; 1996-209351/21.
N-PSDB; AAT28293.
                                                                                                                 Pierce
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US DEPT HEALTH & HUMAN SERVICES
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16-JAN-1991;
08-AUG-1991;
12-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors. It contains a number of phosphorylation sites in common with IRS-1, showing the 2 proteins to be related. IRS-2 can be obtd. e.g. by affinity purification from insulin-stimulated FDC-P2 cells using immobilized SH2 domains of p85, or can be expressed in transformed host cells carrying an encoding cDNA sequence (AAT28293). Cells or animals having the IRS-2 transgene can be used to study insulin-related disorders, e.g. type II disabetes. IRS-2 can be used to raise antibodies and for drug
                                                                                                                                                                                                            APC gene; Adenomatous Polyposis Coli gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumour; adenoma; carcinoma; corcrer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; splice variant.
                                                                                                                                                                                                                                                                                                         Human APC
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91GB-0000975.
91GB-0000975.
91US-0741940.
94US-0289548.
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                                                                                                 95US-0450582
                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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22.2%;
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0; Mismatches
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Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93;
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(ICIL) (UYJO) (UTAH) (CANC-)

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CC The invention relates to a novel method for detecting Adenomatous CC Polyposis Coli (APC) protein in a sample. The method involves CC contacting the sample with antibodies which specifically binds to the CC 2843 amino acid form of the human APC protein, or to a mutant APC Protein, and detecting an APC-antibody complex. Mutations in the APC CC gene play a role in tumorigenesis, indicating that it is a tumour CC the FAP (familial adenomatous polyposis) locus. FAP is an autosomal CC duminant inherited disease in which affected individuals develop CC bundreds to thousands of adenomatous polyps in the colon and rectum, CC some of which progress to malignancy. The FAP locus is often found to CC thromosome 5q deletions have also been observed in tumours of the lung, CC breast, colon, rectum, bladder, liver, sarcomas, stomach, and prostate, colon, rectum, bladder, liver, sarcomas, stomach, and prostate, CC serum of the renes such as FER, TBJ, TBJ, and MCC, it is thought that mutations in the APC gene play a key role in the development of FAP and CC serum or a tumour sample. The method is useful for detecting APC protein and its CC genes, and for testing therapeutic agents for the ability to suppress contains. The present sequence represents a 2742 amino acid splice contains call and no acid variant (AMB23011).
                                                                                                                                                                                                                                                                                                                           Query Match 5.9
Best Local Similarity 22.3
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting Adenomatous Polyposis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that specifically bind to APC protein and detecting the complex formed -
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                                                                                                                                                                                                                    st----kssgsgkmsy 2265
                                                                                                                                     lktpaskspsegqtat-tspr------gakpsvk--selspvar-qtsqigg 2193
                                                                                                                                                                                                                                                              pdqeekpftsnkgprilkpgekstletkkieseskgikggkkv--ykslitgkvrs----
                                                                                                                                                                                                                                                                                           PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid variant (AAB23011).
                                                ASQQVQRNRGNAKSLY 329
                                                                          sskapsrsgsrdstpsrpagqplsrpigspgrnsispgrngisppnklsqlprtsspsta 2253
                                                                                                        DSGSPPKNA---STPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPPQPAFVARTASKYSA 313
                                                                                                                                                                     ITQMILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAYR
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UNIV JOHNS HOPKINS.
UNIV UTAH.
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H, White RL,
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                                                                                                                                                                                                  ------mkqplqa-nmpsisrgrtmihipgvrnsssstspvskkgpp
                                                                                                                                                                                                                                                                                                                        5.9%; Score 103; DB 21; Length 2: 22.3%; Pred. No. 4; tive 46; Mismatches 107; Indels
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, Thliveris A, Nakamura Y, Vogelstein B;
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             DNA encoding protein binding to alpha-fetoprotein gene enhancer useful for prodn. of biological active protein
                                                           WPI; 1992-176828/22.
N-PSDB; AAQ24828.
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Matches 44
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fetoprotein gene. The DNA encoding this protein may be useful for
the prodn. of biologically active proteins by inserting the DNA into
an expression vector and co-transfecting animal cells with another
expression vector in which a gene for the biologically active protein
is placed under the control of alpha-fetoprotein gene enhancer and
                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                       AAR23963;
                                                                                                                                                                                                                                                                                                                                                                                                          AAR23963 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 7;
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                                                                                                                                 /label= zinc-finger 306..366
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171..203
                   /label-
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                                       /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 103; DB 13; Length 2783; 28.0%; Pred. No. 4.1;
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                                                          ∟= zinc-finger
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Best Local Similarity
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                                                                     AAB82946;
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N-PSDB; AAQ24829.
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                                                                                         AAB82946 standard; Protein;
                                                                                                                                                                                                                                                                                                                 Sequence
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/label= zir
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This protein sequence is as the sequence given in AAR23962 except that Ala at position 2460 is replaced by Val.

This protein specifically binds to the enhancer of the alphafetoprotein gene. The DNA encoding this protein may be useful for the prodn. of biologically active proteins by inserting the DNA into an expression vector and co-transfecting animal cells with another expression vector in which a gene for the biologically active protein is placed under the control of alpha-fetoprotein gene enhancer and
Androgen receptor trapped protein; ART; human; transcriptional coregulatory protein; antagonist;
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                                                                                              Human androgen receptor trapped protein
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/label= zinc-finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 103; DB Pred. No. 4.1;
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                                                                                                  (ART).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 44;
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AAR63508 standard; Protein;

2842

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proteins, regilating androgen-dependent gene expression. To identify proteins that interact with the androgen receptor N-terminus, a modified yeast two-hybrid system that allowed the identification of factors expressed in the prostate and which associated with transcriptional activators was used. An androgen-stimulated LNCap prostate cancer cell cDNA library fused to the LexA DNA binding composition of the co
                                                                                                                                                                                          1511
                                                                                                                                                                                                                                                                                                                                                                      1454
1559 qlvslpslpqpppqapppqcplpq-sspspsqlshlp 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of a novel human androgen receptor trapped protein (ART), which belongs to a new class of proteins that interact with the N-terminus of the androgen receptor as androgen receptor transcriptional coregulatory (i.e. coactivator)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 31; Page 99-107; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Garabedian M, Taneja S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New androgen receptor transcriptional coregulatory proteins that interact with androgen receptor to regulate androgen-dependent gene expression, useful for producing antibodies to treat androgen dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-MAR-2000;
15-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    171 SIDLME------SPLPNLSGEALSPTA--TAKDEITQMILKSAARSELGMYVSKRQ 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNY ) UNIV
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                                                                                                                                                                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                         KNASTPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPP 299
                                                                                                                                                                                                                                                                                                                                                   smdameiltptssscstpmpsqaysapapsanntassaflql---taeaeelatfnskte 1510
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2000US-225618P.
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28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 103; DE
Pred. No. 4.1;
                                                                                                                                                                                                                                                             ------KPVLQSISEMKPVMEFHTPMAYRDSGSPP 262
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Matches Query Match Best Local

l Similarity 57; Conserv

Conservative

46; Mismatches

5.9%; 22.3%;

Score 103; Pred. No. 4.

ДВ . 2; 107; 15;

Length 2842; Indels 46;

Gaps

2151

pdgeekpftsnkgprilkpgekstletkkieseskgikggkkv--ykslitgkvrs---- 2204 PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138

GPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNL--SGEALSPTATAKDE 196

79

139

RESULT 1

Qy Ъ δÃ В

197

ITQMILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAYR 256

-----mkqplqa-nmpsisrgrtmihipgvrnsssstspvskkgpp 225

AAQ72297 is a cDNA isolated from the human adenomatous polyposis coli (APC) gene, it encodes the tumour repressors described in AAR63507 and AAR63508. Determination of alterations in APC or its expression products, can be used for the diagnosis and prognosis of cancer e.g. colorectal, lung and breast tumours; and for determining predisposistion to certain cancers such as familial adenomatous polyposis (FAP) and Gardner's syndrome. The wild type APC gene (or a part of it) can be used therapeutically to restore gene function, while primers and probes derived from the cDNA (AAQ72333-400 and AAQ7244-568) can be used to detect mutations. Also APC proteins or analogues can be administered to compensate for a defective gene, and epithelial cells, or transgenic animals carrying a mutated APC allele are useful for detecting therapeutic agents able to suppress tumorigenesis. 16-JAN-1991; 16-JAN-1991; 16-JAN-1991; 16-JAN-1991; Sequence Claim 3; Columns 71-84; 113pp; English. (CANC-) (ICIL ) (UYJO ) (UTAH ) WPI; 1994-316233/39. N-PSDB; AAQ72297. Albertsen H, Anand R Joslyn G, Kinzler K, Vogelstein B, White Adenomatous polyposis coli; tumour repressor; Gardner's syndrome; familial adenomatous polyposis; cancer diagnosis and prognosis; tumorigenesis suppression. prognosis and treatment of cancer New human adenomatous polyposis coli repressor and derived primers and 08-AUG-1991; US5352775-A. Homo sapiens. Adenomatous 23-MAY-1995 IMPERIAL CHEM IND. UNIV. JOHNS HOPKINS CANCER INST UNIV UTAH 2842 AA; polyposis coli Anand R, Carlson M, inzler K, Markham AF, (first entry) 91GB-0000962. 91GB-0000963. 91GB-0000974. 91GB-0000975. White RL; 91US-0741940 tumour repressor. Groden J, | Nakamura Y, probes DNA encoding tumour for diagnosis Hedge PJ; , Thliveris ?

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RESULT 15
AAR2602
ID AAR260
AC AAR26
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                                                                                                                                                                                                                     Query Match 5.9%; Score 103; DB 13; Length 2843; Best Local Similarity 22.3%; Pred. No. 4.2; Matches 57; Conservative 46; Mismatches 107; Indels 46
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2252 lktpaskspseggtat-tspr----
                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence is encoded by the APC (Adenomatous Polyposis Coli) gene associated with tumorigenesis, found on chromosome 5q.
The sequence may be mutated by deletions insertions, inversions, or point mutations of the gene. The APC gene is expressed in most normal tissues as well suggesting that APC is a tumour suppressor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of somatic and germ-line alterations of human APC - used to diagnose, treat and study familial adenomatosus polyposis and sporadic colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2294 skapsrsgsrdstpsrpaqqplsrpiqspgrnsispgrngisppnklsqlprtsspsta 2353
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Joslyng, Kinzler KW, Markham A, Nakamura Y,
Vogelstein B, Whiterl, Markham AF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neoplasm; cancer; oncogene; tumour; growth; detection; diagnosis;
prognosis; treatment; sporadic colorectal carcinomas; ss.
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                                                                                             2152 pdgeekpftsnkgprilkpgekstletkkleseskgikggkkv--ykslitgkvrs---- 2205
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 47; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-284685/34.
N-PSDB; AAQ27234.
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(ICIL ) IMPERIAL CHEM IND PLC.
(UYJO) UNIV JOHNS HOPKINS.
(UTAH ) UNIV UTAH.
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08-AUG-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JAN-1993 (first entry)
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PFLEROPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138
                                                                                                                                                                                                                                                                                                                                                                                           2843 AA;
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91US-0741940.
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Thliveris A;
                                                                                                                                                                                                                               Indels 46;
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Search completed: September 16, 2002, 00:42:28 Job time: 3377 sec

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Minimum DB
Maximum DB
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                             116
103.5
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                                                                    seq
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length: 2000000000
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Match
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2: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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Gapop 10.0 , Gapext 0.
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Listing first 45 summaries
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1734
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                    DB
                   PCT-US95-03747-2
US-08-317-310A-64
US-07-741-940-7
US-08-289-548A-7
US-08-289-548A-2
US-08-452-6548-2
US-08-452-6548-2
US-08-452-6558-7
US-08-452-6588-7
US-08-452-6588-7
US-08-452-6588-7
US-08-452-6588-7
US-08-452-6588-7
US-08-452-1355A-7
US-09-03-687A-7
US-09-03-687A-7
US-09-03-687A-7
US-09-0442-100-4
US-09-442-100-4
US-08-217-327-6
US-08-188-582-13
US-08-646-715-13
US-08-646-715-13
US-08-646-715-13
US-08-93-674A-5
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Sequence 64, Appli
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                                                                                                                         Query Match
Best Local Similarity
Matches 54; Conserv
                                                                368
                                                                                         140 PEPHLAGDRPSKHLKLVFIRHCLRALRLPR-----ISIDLME-----SPLPNLS 183
 425 AEA--PRTILEFE-TQSIVPPLGSSEEEGKVLEQEEKYRGEEEKEEEEEEEEVEDEALWA 481
                             184 GEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFYLRRARRRRK-----FA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: California
                                                           PASHLASDALE - - - AIVTVTETLEELKLPQEAVESESRGAIYSIPIIEDGGGGSSTPEDP 424
                                                                                                                         Conservative
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Result No.

45	44	43	42	41	40	39	38	37	36	ω 5	34	ω ω	32	ω	30	29	28
91	91	91.5	92	92.5	92.5	92.5	92.5	92.5	92.5	92.5	93	93	93	94	94	94	94
5.2	5.2	5.3	5.3	5.3	5 3	5.3	5.3	5.3	5.3	5.3	5.4	5.4	5.4	5.4	5.4	5.4	5.4
345	345	1464	404	1298	1298	1298	739	739	737	737	560	560	560	1017	666	666	666
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US-09-059-520A-1	US-08-843-993-1	US-08-891-640-2	US-09-232-468A-8	US-08-843-659-2	US-09-259-821A-2	US-08-690-473-2	US-09-001-951-24	US-09-035-648-24	US-08-646-715-16	US-08-188-582-16	US-08-470-339-194	US-08-470-335-194	US-08-341-018-58	US-09-600-776-6	US-08-532-384-17	US-08-346-128-36	US-08-083-590A-17
Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 8, Appli	'n	2	2, A	Sequence 24, Appl	Sequence 24, Appl	Sequence 16, Appl		Sequence 194, App	Ξ.		Sequence 6, Appli		Sequence 36, Appl	Sequence 17, Appl

ALIGNMENTS

Title:

Run

on:

## TELEPHONE: (619) 535-9001 TELEPAX: (619) 535-9949 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 912 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein Sequence 2, Application PC/TUS9503747 GEMERAL INFORMATION: APPLICANT: LA JOLLA CANCER RESEARCH FOUNDATION TITLE OF INVENTION: Brevican, A Glial Cell Proteoglycan NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite 700 CTIY: San Diego COUNTRY: USA ZIP: 92122 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V CLASSIFICATION: ATTORREY/AGENT INFORMATION: NAME: Imbra, Richard J. REGISTRATION NUMBER: 37,6 REFERENCE/DOCKET NUMBER: CURRENT APPLICATION DATA: APPLICATION NUMBER: PC: FILING DATE: 27-MAR-199 TELECOMMUNICATION INFORMATION: 27-MAR-1995 Release #1.0, Version #1.25 PCT/US95/03747 37,643 FP-LJ 1453

; Score 116; DB 5; Length 912; Pred. No. 0.0047; 26; Mismatches 101; Indels

101; Indels 42; Gaps

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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 22.2
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: JDP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEPAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 1321 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 64, Application US/08317310A Patent No. 5858701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/317,310A
FILING DATE: 03-OCT-1994

CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Louis Myers
REGISTRATION NUMBER: 35,965
REGISTRATION NUMBER: 35,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -08-317-310A-64
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APPLICANT: SUN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PIERCE, Jacalyn H.
TITLE OF INVENTION: THE IRS FAMILY OF GENES
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLECULE . amino acid
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 KTLPTPREGNLASPPPSTLVGAREIEEETGGPELSGAPRGESE 584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 WPSELSSLDPEAPLPTEPVPEESLTQASPPVRAALQPGVSPPPYDEPEAPRPPRVLGPPT 541
                263 KNA---
                                                       909 -----GEYIN----IDFGEAGTRLSPPAPPLLASAASSSSLLSASSPASSLGSGTPG 956
                                                                                                                                                                                                               842 -----GAAGGSHTQ----PHHSAVPS-----SMR-----PSAIGGRP 869
                                                                                                                                                                                                                                                                                            806 SCS-----GDNDQYVLMSSP---VGRILEEERLE-----PQATPGAGTF----- 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 RSSPPPKN----VSPPPQPAFVARTASKYSAASQQVQRNRGNAK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 WKPVLQSISEMKPVMEFHTPMAYRDSGSPPKNA-----STPSLPGPKNISPPRQVSVPQ 286
                                                                                           203 KSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAYRDSGSPP 262
                                                                                                                                                                         150 SKHLKLVFIRHCLRALRLPRISID------LMESPLPNLSGEALSPTATAKDEITQMIL 202
                                                                                                                                                                                                                                       30 SCSVHDLLLGNPDYYVCGSTPYTITNRMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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PREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NO. 5850, L.
INFORMATION:
LICANT: WHITE, MOTTIS F.
LICANT: SUN, Xiao Jian
Tacalyn F
                                                                                                                                   EG-----FLGQRCRAVRPTRLSLEGLQTLPSMQEYPLPT---EPKSP------
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                                                                                                                                                                                                                                                                                                                                                                      6.0%; Score 103.5; DI 22.2%; Pred. No. 0.14; tive 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JDP-022
              -----ISPPRQVSVPQRSSPPPKN 294
                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                        93; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 1321;
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US-07-741-940-7
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Patent No.
GENERAL II
                                                                                                                                       Query Match 5.9%; Score 103; DB 1; Length 2842; Best Local Similarity 22.3%; Pred. No. 0.49; Matches 57; Conservative 46; Mismatches 107; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/741
FILLING DATE: 1920109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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APPLICANT:
APPLICANT:
                                                            2151 PDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKV--YKSLITGKVRS----
                                                                                                                                                                                                                                                                          ORGANISM: Homo
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2842 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1015 TSPSSLQQPLPPAPGDLYRLPPASAATSQ 1043
139 GPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNL--SGEALSPTATAKDE 196 ::| : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     957 TSSDSRQRSPLSDYMNLDFSSPKSPKPSTRSGDTVGSMDGLLSP--EASSPYPPLPPRPS 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 VSP------PPQPAFVARTASKYSAASQ 316
                                                                                     79 PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138
                                                                                                                                                                                                                                                               CLONE:
                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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5. 5352775
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HEDGE, PHILIP J.
JOSLYN, GEODE
KINZLER, KENNETH
KARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Banner, Birch, McKie & Beckett
1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                        2842 amino acids
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                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US/07/741,940
                                                                                                                                           46; Mismatches 107; Indels 46;
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                                                                                                                                           Gaps
                                                              2204
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2205 -- NSEISGQ------MKQPLQA-NMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPP

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US-08-289-548A-7
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Query Match 5.9%; Score 103;
Best Local Similarity 22.3%; Pred. No. 0.
Matches 57; Conservative 46; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/289
FILLING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
                                                                                                                                                                                                                                                                                            TELEPHONE: 202-508-9100
TELEPHAX: 202-508-929
TELEPAX: 202-508-929
TELENATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2842 mino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORPORT APPLICATION DATA:

CORPOTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: THIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                               ORGANISM: HOMO IMMEDIATE SOURCE:
                                                                                                                                                                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2354 ST----KSSGSGKMSY 2365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2294 SSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTA 2353
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                        TOPOLOGY:
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1001 G Street, NW
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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HEDGE, PHILIP J.
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                                                                                                                                                                       Homo sapiens
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    Mismatches
                     DB 1; Length 2842;
0.49;
107; Indels
  46;
Gaps
  11;
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                                                                                                                                                             APPLICATION NUMBER: US/08/452
FILING DATE: 25-MAY-995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/741
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                            TELEFAX: 202-508-9299:
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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ADDRESSEE: Banner, Birch, McKie 6 Beckett
STREET: 1001 G Street, NW
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APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: THLIVERIS, ANDREW
APPLICANT: THLIVERIS, ANDREW
APPLICANT: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
ANDRESS OF COLOREGES OF A
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APPLICANT:
APPLICANT:
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    MOLECULE TYPE:
                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257
                                      TYPE: amino acid
STRANDEDNESS: si
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                                                                                 LENGTH:
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GRODEN, JOANNA
HEDGE, PHILIP J.
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ANAND, RAKESH
  protein
                                        single
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; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: APC
US-08-452-654-7
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COUNTRIE USA

ZIP: 20001-4598

COMPUTER READABLE FORM.

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC compatible

OPERATICS SYSTEM: PC-DOS/MS-DOS

SOPTWARE: PSTEM: PC-DOS/MS-DOS

SOPTWARE: PSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/741,940

FILING DATE: 19920109

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 32,141
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
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CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ST----KSSGSGKMSY 2365
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HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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1001 G Street, NW
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Best Local Similarity
Matches 57; Conserv
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APPLICANT: ALBERT
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APPLICATION NUMBER: US/08/289
FILING DATE: 12-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGESTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, LTD
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKANURRA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
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HEDGE, PHILIP J.
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                                                                                                                                              US/08/289,548A
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                       1107.46943
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US-08-452-654-2
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Best Local Similarity
Matches 57; Conserv
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
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MOLECULE TYPE:
                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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CITY: Washington
                                                                     APPLICATION NUMBER: US/0 FILING DATE: 25-MAY-1995
APPLICATION NUMBER: US 07/741,940 FILING DATE: 08-AUG-1991
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GRODEN, JOANNA
HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLITUERIS, ANDREW
                                                                                                                                                                                                                                                                                                        E: Banner, Birch, McKie & Beckett
1001 G Street, NW
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                                                                                            US/08/452,654
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TOPOLOGY: linear; MOLECULE TYPE: protein: US-08-452-654-2
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US-08-452-655B-2
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Patent No. 5783666
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Best Local Similarity
Matches 57; Conserv
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APPLICANT:
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LENGTH: 2843 amino acids
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: THILIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF A
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
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ADDRESSEE: Banner & Witcoff, Ltd
STREET: 1001 G Street, NW
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                                                                                                                                                                          CITY: Washington STATE: D.C.
APPLICATION NUMBER:
                                                                                                                                    COUNTRY: USA
ZIP: 20001-4598
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HEDGE, PHILIP J.
JOSLYN, GEOFF
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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  US/08/452,655B
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CLASSIFICATION:

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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2843 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.9%; Score 103; DB 1; Length 2843; Best Local Similarity 22.3%; Pred. No. 0.49; Matches 57; Conservative 46; Mismatches 107; Indels 4
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APPLICATION NUMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERRACE/DOCKET NUMBER: 1107.49964
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08452655B Patent No. 5783666
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                                                                                                                      TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                        CORRESPONDENCE ADDRESS:
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                STREET: LVC
CITY: Washington
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COUNTRY:
                                                      ADDRESSEE: Banner & Witcoff, Ltd
STREET: 1001 G Street, NW
                                                                                                                                                                                      HEDGE, PHILIP J.
JOSLYN, GEOFF
KINZLER, KENNETH
MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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12-AUG-1994
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; MOLECULE TYPE:
; HYPOTHETICAL: )
; ANTI-SENSE: NO
US-08-452-655B-7
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US-08-370-235A-2
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Best Local S
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APPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/289,548
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/741,940
PRIOR APPLICATION UMBER: US 07/741,940
PRIOR APPLICATION UMBER: US 07/741,940
FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
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TELEFAX: 202-508-929
INFORMATION FOR SEQ ID NO: 7:
                                      GENERAL INFORMATION:

APPLICANT: VOGELSTEIN, BERT
APPLICANT: KINZLER, KENNETH W.
APPLICANT: HILL, DAVID E.
APPLICANT: JOHNSON, KAREN A.
TITLE OF INVENTION: ANTIBODIES AND ASSAYS FOR DERMINING
TITLE OF INVENTION: MUTATIONS IN THE APC GENE
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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CORRESPONDENCE ADDRESS:
                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 GPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNL--SGEALSPTATAKDE 196
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICANT: CARLSON, MARY
APPLICANT: CARLSON, MARY
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, PHILIP J.
APPLICANT: JOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: THLIVERIS, ANDREW
TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
APPLICANT:
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REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508 9100
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CITY: WASHINGTON
STATE: DC
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ALBERTSEN, HANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches 107; Indels 46;
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US-08-450-582-7

Sequence 7, Application US/08450582

Patent No. 6114124

GENERAL INFORMATION:
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APPLICATION NUMBER: US 08/452,655

FILING DATE: 25-MAY-1995

APPLICATION NUMBER: US 08/289,548

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/741,940

FILING DATE: 08-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: KAGAN, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 1107.49964
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INFORMATION FOR SEQ ID NO: 2:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, NW
                                                                                                                                                         2355
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LENGTH: 2843 amino aci
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                      2295 SSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTA 2354
                                                                                                                                                                                                                                                                                                                                                                                                                2206 --NSEISGQ------MKQPLQA-NMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPP 2252
                                                                                                                                                                                              314 ASQQVQRNRGNAKSLY 329
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CLASSIFICATION: 435
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CITY: Washington
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                                                                                                                                                      ST----KSSGSGKMSY
                                                                                                                                                                                                                                                                   DSGSPPKNA---STPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPPQPAFVARTASKYSA 313
                                                                                                                                                                                                                                                                                                                                                                        ITQMILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAYR 256
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APPLICANT:

ALBERTSEN, HANS ANAND, RAKESH

2294

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; TOPOLOGY: 1in; MOLECULE TYPE: ; MOLECULE TYPE: ; HYPOTHETICAL: Y ANTI-SENSE: NO US-08-450-582-7
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SEQUENCE 2843 mnino acids
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COMPUTER READABLE FORM:
MEDIJM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/450,582
FILING DATE:
2295 SSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTA 235
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/452,655
FILING DATE: 25-MAY-1995
                                                                                                                                                                                         2206 --NSEISGQ-----MKQPLQA-NMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPP 2252
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FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 08-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 11
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TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 102
                                                                                                2253 LKTPASKSPSEGQTAT-TSPR--
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                                                                                                                                         197 ITQMILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEEHTPMAYR 256
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                                             257 DSGSPPKNA---STPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPPQPAFVARTASKYSA 313
                                                                                                                                                                                                                                       139 GPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNL--SGEALSPTATAKDE 196
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STRANDEDNESS: si
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1001 G Street, NW
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MARKHAM, ALEXANDER F.
NAKAMURA, YUSUKE
THLIVERIS, ANDREW
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JOSLYN, GEOFF
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                                                                                                                                                                                                                                                                                                                                                                                      46; Mismatches 107; Indels 46;
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                                                                                           ---GAKPSVK--SELSPVAR-QTSQIGG 229
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US-08-821-355A-7
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                                                                                                                                                                                                           Best Local Similarity Matches 57; Conserv
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 amino aci
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
MOLECULE TYPE:
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MEDIUM TYPE: Diskett
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2253 LKTPASKSPSEGQTAT-TSPR---
                                                                     2206 --NSEISGQ----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 20-MAR-
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                 197 ITQMILKSAARSELGMYVSKRQEFYLRRARRRRKFAWKPVLQSISEMKPVMEFHTPMAYR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                   139 GPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNL--SGEALSPTATAKDE 196
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                                                                                                                                                                          79 PFLEROPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                          5.9%; Score 103; DB 2; Length 2973; illarity 22.3%; Pred. No. 0.52; Conservative 46; Mismatches 107; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Sparks, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinzler, Kenneth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clevers, Hans
Korinek, Vladimir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barker, Nick
                                                                                                                                                                                                                                                                                                                                     linear
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20-MAR-1997
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US-09-003-687A-7
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                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMB UT
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                    Query Match 5.9%; Score 103; DB 2; Length 2973; Best Local Similarity 22.3%; Pred. No. 0.52; Matches 57; Conservative 46; Mismatches 107; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Applic
Patent No. 5998600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/821,355
FILING DATE: 20-MAR-11997
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REGISTRATION NUMBER: 1107 05
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,687A
FILING DATE:
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APPLICANT: Sparks, Andrew
TITLE OF INVENTION: Beta Catenin, TCF-4, and APC
TITLE OF INVENTION: Interact to Prevent Cancer
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
2206 --NSEISGQ------MKQPLQA-NMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPP 2252
                                                                                   2152 PDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKV--YKSLITGKVRS----
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APPLICANT: Clevers, Hans
APPLICANT: Korinek, Vladimir
APPLICANT: Morin, Patrice
APPLICANT: Morin, Fatrice
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CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
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                                                                                                             79 PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNE 138
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Search completed: September 16, 2002, 00:43:15 Job time: 2724 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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 Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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I49505
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T18535
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A41948
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T18860
T33659
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(without alignments)
742.080 Million cell updates/sec
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## ALIGNMENTS

hypothetical protein DKFZp434B034.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-C;Accession: T12533
State: C;Accession: T12534
A;Accession: T12533
A;Accession: T12533
A;Accession: T12533
A;Accession: T12534 C; Genetics: A; Note: DKF A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <AMAN
A;COSS-references: EMBL:AL096728
A;Experimental source: adult testis; clone DKFZp434B034 Query Match Best Local S Matches 78 199 110 294 312 260 257 208 167 161 TNWVARRGSSAGRKV------SCAPPSMQPPAPPAELAAPLPSP------101 NYGSPYHVNHNANYSSMPSPDMDPADRRQPEQARRPLSVATDNMMLEFYKKDGMGVMVMD 160 56 RMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVHR-----GSKILPRFSKHGVHVRELR 109 42 MTPSNMAIVLG-PNLLWPQABGNITEMMTTVSLQIVGIIEPIIQHADWFFPGEIEFNITG 3 LTPFSCVTVQGYVRVVYP--DGHVENLSKSCSVH-----DLLLGNPDYYVCGSTPYTITN 55 DKFZp434B034.1 RQRPTLPPPQPPTVNLSAS 390 ---NVSPPPQPAFVARTAS 309 QPSPVSLSPTPPSTPSPYGLSYPQGYSLASGQLSPAAAPPLASPSVFTSTLSKSRPTPKP 371 SPPK---NASTPSLPGPKNISPPRQVSVP-------QRSSPPPK- 293 PGAQPGAQPGASPSSQPPADQSPHTLRK-----VSKKLAPIPPKVPFGQPGAMADQSAG -----SELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTP--MAYRDSG LPEQPLDSPAAPALSPSGLGLQPGPERTSTTKSK--ELSPGSAQKGSPGSSQGTACAGTQ LPRISIDLMESPLPNLSGEALSP----TATAKDEITQMILKSAAR------S---PTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALR 166 ch 7.6%; Score 131; 1 Similarity 20.6%; Pred. No. 0. 78; Conservative 57; Mismatche Mismatches 23-Jul-1999 #text\_change 23-Jul-1999 DB 2; Length 413; ).017; 142; Indels 102; Gaps 100 311 259 256 198 207 15;

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R:Mueller, W.E.G.
submitted to the EMBL Data Library, April 1997
A;Reference number: Z20501
A;Accession: T28666
A;Accession: T28666
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C:Accession: E96654

C:Accession: E96654
                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1102 <MUE>
A;Cross-references: EMBL:Y13104; NID:e1289874; PID:e316788; PIDN:CAA73558.1
A;Cross-references: EMBL:Y13104; NID:e1289874; PID:e316788; PIDN:CAA73558.1
                                                                                                                                                                                                                                                                                                                           protein kinase C-related kinase PRKSD - Suberites domuncula C;Species: Suberites domuncula C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000 C;Accession: T28666
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A; Map position:
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A;Molecule type: DNA
A;Residues: 1-796 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 TPQSQSQSPQHHQQQSQSPQHPNQNQTVSFQNQQLP-FQLHQPHFAQAVQTQSQSQQQRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 TPNAQ-----PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFDYHSVTMQQLESIRNEGPEPHLAGD-----RPSKHLKLVFIRHCLRALRLPRISIDLM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFPLSQPPSNSKPFPMSQSSQNSKPFPVSQSSQKSKPLLVSQSSQRSK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PORSSPPPKNVSP------PPQPAFVARTASKYSAASQQVQRNR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEAAQLSLLPSVSDSS-----HASQPTRSNQSHAVSKPQPVSKPHPPFPMSQPPP--TSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPPSRSFEG---SSHRTPSTELTWASKPTPVSEPVRHSELVPWQYSEPARQYQL--SSRS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QFDQQLLQEQQQASWRQQVGQEHSSGSSGDWKRPVEEVRLINLNNATERVQSSRRFAEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKFAWKPVLQSISEMKPVMEFHTPMAYRDSG----SPPKNASTPSLPGPKNISPPRQVSV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESPLPNLSGEALSPTATAKDEIT-----QMILKSAARSEL--GMYVSKRQEFYLRRARRR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68;
                                         Similarity
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                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.2%; Score 124; DB 2; Length 796; 23.6%; Pred. No. 0.14;
                                         25.8%;
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                     36;
                   Score 118.5;
Pred. No. 0.54
36; Mismatches
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                                                            DB 2;
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                        149;
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                     Indels
                                                            Length 1102;
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                     59;
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Dewar, K.;
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  VP----
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78; Conserv
  -SSPVQ---
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protein kinase kin1 - fission yeast (Schizosaccharomyces pombe)
C.Species: Schizosaccharomyces pombe
C.Species: Schizosaccharomyces pombe
C.Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000
C.Accession: T40503
R.Gwilliam, R.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, September 1998
A; Reference number: Z21933
A; Accession: T40503
A; Accession: T40503
A; Accession: T40503
A; Accession: T40503
A; Molecule type: DNA
A; Residues: 1-891 <GWI>
A; Residues: 1-891 <GWI>
A; Residues: 1-891 <GWI>
A; Residues: 1-891 <GWI>
A; Residues: September 1988
A; Residues: 1-891 <GWI>
A; Reperimental source: strain 972h-; cosmid c4F6
C; Genetics:
A; Gene: SPDB:SPBC4F6.06
A; Map position: 2
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase 560 TSGGSTPKSPITPTSPPYFDHSGRKRSLQENGGDL-PPPIP-MSEEDL--IVGAPHSATE 372 LSRMLVTDPLKRATLEEVLNHPWMIRNYEGPPASFAPERSP----------------------------------412 322 VDVWSFGIVLYVLVCGKV-PFDDQNMSALHAKIKKGTVEYPSY-----LSSDCKGL 371 262 VVHRDLKIENILISKTGDIKIIDFGLSNLYRRQSRLRTFCGSLYFAAPELLNAQPYIGPE 616 PII-PPPREFLGGSVSSTDE---HRVDDNIGPPPKFIMESWSAVSPTHRHTSPQHQKPRD 200 MILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAY--RD 144 LAG----DRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNLSGEALSPTATAKDEITQ 199 61 -EVLEYGVTYFVCATPNAQPFLERQPKVVH----RGSKILPRESKHGVHVRELRSPTHGS 115 17 VVYPDGHVEN--LSKSCSVHDLLLGNPDYY------VCGSTPYTITNRMAAE---------RH----TELNTDIVTWARLLNRSAPSTHTDPHISSPMVISTQDKSSKQESPPHSPH TGREYNTVISPPPTRESVPAPTRSPAHQVFPPPPNPSFPTPLS-PSRVAPLPPISQPPPA 730 PRESKHGVHVRELRSP--THGSQQSRKVFDYHS-----VTMQQLESIRNEGP--EPH 143 LPGPKNISPPRQVSVPQRSSPPPKNVSPPPQPAFVARTASKYSAASQQVQRNRGNAK QQSRKVFD-YHSVTMQQLES----IRN-EGPEPHLAGDRPSKHLKLVFIRHCLRALRLPR 169 SG-----SPPKNASTPS-----LPGPKNISPPRQVSVPQRSSPPPKNVSPPPQ 300 FRIRHAAHDIENPILPSLSMNTDIYDAFHPLISIYYLVSERRVYEKGGNWNRIAKTPVSS RRARRRKFAWKPVLQSISEMKPVMEFHTPM------AYRDSGSPPKNASTP--S 269 ITLPLDPEIIREMNGFDFGPPEKIVRELTKVISSEAYQSLAKTGFYSGPNSADKKKSFFE 472 ISIDLMESPLPNLSGEALSPTATAKDEITQMILKSAARS--ELGMY-----VSKRQEFYL 222 LYLRLEDYFDTNGATYCLP--LEPQGILLVEVTYEFPKTERRQPKLKRGKRIFRRG-KVL 6.7%; Score 117; DB 2; Length 891; ilarity 21.8%; Pred. No. 0.53; Conservative 50; Mismatches 137; Indels -PTSYNRTLPPMPEVV - - - AYKGDEESPRVSRNTSLAR GSPDB:GN00067; SPDB:SPBC4F6.06 92; protein kinase 573 326 Gaps 95 60 671 257 519 559 507 17;

hom

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protein kinase 1 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_char
C;Accession: A38903, A36474
R;Levin, D. E.; Bishop, J. M.
submitted to GenBank, May 1991
A;Reference number: A38903
A;Accession: A38903
A;Accession: A38903
A;Molecule type: DNA
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C;Genetics:
A;Gene: kin1+
C;Superfamily:
C;Keywords: ATP
F;123-395/Domai
F;131-139/Regio
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A; Residues: 1-991 < LEV>
A; Cross-references: GB: M64999; NID: g173409; PIDN: AAA63577.1; PID: g173410
A; Cross-references: GB: M64999; NID: g173409; PIDN: AAA63577.1; PID: g173410
R; Levin, D.E.; Bishop, J.M.
Broc. Natl. Acad. Sci. U.S.A. 87, 8272-8276, 1990
A; Title: A putative protein kinase gene (kin1(+)) is important for growtle A; Reference number: A36474; MUID: g1045979
A; Accession: A36474
A54423

A54423

Drevican precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 21-

C:Accession: A54423; 541914

R:Yamada, H.; Watanabe, K.; Shimonaka, M.; Yamaguchi, Y.

J. Biol. Chem. 269, 10119-10126, 1994

A:Title: Molecular cloning of brevican, a novel brain proteoglycan

A:Reference number: A54423; MUID:94193597

A:Accession: A54423

A:Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol
:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
:123-395/bomain: protein kinase homology <KIN>
;131-139/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:M36060
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                                                                                                                                                                                                                                                                                                                                                                                    FRIRHAAHDIENPILPSLSMNTDIYDAFHPLISIYYLVSERRVYEKGGNWNRIAKTPVSS
                                                                                                                                                                                                                                                                                                                                                                                                                             RRARRRKFAWKPVLQSISEMKPVMEFHTPM------AYRDSGSPPKNASTP--S 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVHRDLKIENILISKTGDIKIIDFGLSNLYRRQSRLRTFCGSLYFAAPELLNAQPYIGPE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVYPDGHVEN--LSKSCSVHDLLLGNPDYY-----VCGSTPYTITNRMAAE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLPLDPEIIREMNGFDFGPPEKIVRELTKVISSEAYQSLAKTGFYSGPNSADKKKSFFE 472
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78; Conservative
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A;Map position: 2
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les 60; Conserv
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hypothetical protein At2g25050 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: F84643 Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, R.;Lin, X.; Kaul, S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tall euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ver Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID: 20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross references: GB:X75887; NID:9452820; PIDN:CAA53481.1; PID:9452821 C;Superfamily: aggrecan; C-type lectin homology; complement factor H reperson F;50-139/Domain: immunoglobulin homology <LMM>
F;174-251/Domain: link protein repeat homology <LNK1>
F;174-251/Domain: link protein repeat homology <LNK2>
F;272-353/Domain: EGF homology <EGF>
F;689-809/Domain: C-type lectin homology <LCH>
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A; Residues: 1-912 < YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-742 <STO>
A;Cross_references: GB:AE002093; NID:g4559347; PIDN:AAD23008.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;816-872/Domain: complement factor H repeat homology <FHD>
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                                                                                                                                                                                                                                                                                                                                                                                                                 52 TITNRMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGVHVRELRSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
QSPVTSPLPNRSPTQGSPASISRFH-----SSPSSLGITSILHDHGSCKDEESTSSS
                                                                                                                                                      IDLMESPLPNLSGEALSPTATAKDEITOMILKSAARSELGM-----YVSKRQEFYLRRA
                                                                                                                                                                                                                        DTSSPEKEK-----DTMSSHKSYAD--PNSILKKVDESRGLRVSVQRNVHSKIFSPRMV
                                                                                                                                                                                                                                                                                  THGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRIS
                                                                                                                                                                                                                                                                                                                                                   TVFNQITAANILQESLDSGSPRSPDSRSLLESALEKVKEKTKLM-----ISENIVSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPSELSSLDPEAPLPTEPVPEESLTQASPPVRAALQPGVSPPPYDEPEAPRPPRVLGPPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFYLRRARRRKK-----FA 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PASHLASDALE - - - AIVTVTETLEELKLPQEAVESESRGAIYSIPIIEDGGGGGSSTPEDP 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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21.7%;
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24.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 114; DB
Pred. No. 0.72;
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Pred. No. 0.66;
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Gnoj, L.;

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submitted to the EMBL Data Library, October 1998
A; Description: The sequence of C. elegans cosmid W07E
A; Reference number: Z21384
A; Areasion: T33558
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A;Cross-references: EMBL:AF100304; PIDN:AAC68911.1; GSPDB:GN00021; CESP:W07B3.2c
A;Experimental source: strain Bristol N2; clone W07B3
                                        A; Molecule type: DNA
A; Residues: 1-539 <WOH>
                                                                                                                                                                                                                         hypothetical protein W07B3.2c - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
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A; Introns: 553/2
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A;Experimental source: strain 972h-; cosmid c23E2
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A; Residues: 1-576 <SKE>
                                                                              Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 LSRP----PPP----PPPPPISSLRSTPSPSSTSNSI 596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 EAT----EIFTHSQPLPIPAGPSSKSHAIDFKFKFPSKSASSLPCSKSNDSMVNICYMLK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 VTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGV-HVRELRSPTHGSQQSRKVFDYH 125
                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSGSPPKNASTPSLPGPKNISPPROVSVPQRSSPP--PKNVSPPPQPAFVARTASKYSAA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SASLYKOPSFNSNPAPITTSSATHTSQF-----STSSSSSVNSVHTPVMVPNPYFQYN 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATISKRYAFLGSSQSAKAELIMVP-PNLAGKPLSANSSFGSSAKTFQLPEFDSVT----P 180
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23.8%;
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A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T10M13.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Fbb-1999 #sequence_revision 19-Feb-1999 #text_change 04-Mar-2000
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A:Gene: CESP:W07B3.2c
A:Map position: 3
A:Introns: 61/3; 101/3; 124/3; 257/3; 291/2; 364/3; 495/3
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C; Superfamily: Arabidopsis thaliana hypothetical protein T10M13.10
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A; Note: T10M13.10
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A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-202 <JOH>
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Best Local
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                                      244 KPVMEFH 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 KLVFIRHCLRALRLPRISID-LMESPLPNLSGEALSPTATAKDEITQMILKSAARSELGM 212
                                                                                                                                                                                                        124 YHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNLS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 LVGNQGN 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     353 LRYQRMTPDQRKSYNQKRYTPKRRRNEMDDMISAGQ----MAVGSSGTITMGTGTPAKKD 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 YVSKRQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPMAYRDSGSPPKNASTPSLPG 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 KRVYNQRRTEAFRRRMEEEMLLAMPIGRINGEAL-----DRAQQIVVRNAKRAEAAR 352
                                                                                                                                                                                                                                                                                           64 EYGVTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFD 123
                                                                                                                                                                                                                                                                                                                                   19 KVVLSDGRVQNLEEETTVAEIMLENPQHVVVEFDPSSISFNNDAKTVKRKLAPLPADKTL 78
                                                                                                                                                                                                                                                                                                                                                                         16 RVVYPDGHVENLSKSCSVHDLLLGNPDYYVCGSTP-----YTITNRMA---AEEVL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                TRSYKNNNPATD-
KAKKKIH
                                                                                                                       GEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFYLRRARRRKFAWKPVLQSISEM
                                                                                                                                                                                                                                                    EPGKIYLV------LPA-KRSGGRAAKSSSAVLTSEEMRKML- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                    54;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KNISPPRQVSVPQR----SSPPPKNVSPPPQPAFVARTASKYSAASQQ 317
                                                                                -TVVAATSVGRLEAEMEEEDRPEFLSRQLSGR---GWKPSLDPIREK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                    6.4%;
21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 111; DB
Pred. No. 0.23
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 111.5; D
Pred. No. 0.74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
. 23;
                                                                                                                                                                 ---FSATAMVRSSFSYYEGILPWFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoffman, J.; Hasegawa, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75;
                                                                                                                                                                                                                                                                                                                                                                                                                    89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
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243 135

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C. Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C.Accession: T46050
R.Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000
                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-1356 <FAV>
A;Cross-references: EMBL:U23515; NID:g746492; PID:g746500; PIDN:AAC46552.1; CESD:R144.7
A;Experimental source: strain Bristol N2
C;Genetics:
                                                                                                                                                                                                                                                                                             A;Reference number: Z23015
A;Accession: T46050
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <RIE>
A;Cross-references: EMBL;AL132965
A;Experimental source: cultivar Columbia; BAC clone
C;Genetics:
                                                                                                                                                                                                                                                       A; Description: The sequence
A; Reference number: Z18571
A; Accession: T16754
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T16754
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c; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
C; Accession: T46050
                                                                                                  A; Gene: CESP:R144.7
A; Introns: 71/1; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 3
A; Introns: 52/1; 83/1; 153/2; 209/1;
A; Note: T16K5.190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 62
Query Match
Best Local S
Matches 70
                                                                                                                                      Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 YPPPQYPQAGYPPAGYPPPQQGYGQGYPAQGYPPPQ 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 ISPPR--QVSVPQRSSPPPK-----NVSPPPQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 TITNRMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVHRGS--KILPRFSKHGVHVRELR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 22.
les 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLRRARRKFAWKPVLQSISEMKPVMEFHTPM----AYRDSGSPPKNASTPS-LPGPKN 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALRLPRISIDLMESPLPNLSGEALSPTATAKDEITQMILKSAAR---SELGMYVSKRQEF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESDIFPSSFHKTPEGRR-----KLTKEELQKFTKESTE-----N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SISRKLLAQRIYEQDDETESCS------PGLIHATSFASPLPRGSNKKLRTVPLS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----RVRYKERNKPSDKSITEKKKKMSYQDPQHPVSAPPPQGYPPKEGYPPAGYPPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALK-----ELVSSPEEGSSGSE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SPTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLR 163
70; Conservative
                                                                                                180/3; 238/1; 256/2; 273/2; 337/3; 528/2; 656/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.3%;
6.2%; Score 108; DB 2; Length 1356; 21.7%; Pred. No. 4.4; tive 46; Mismatches 101; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB 2;
Pred. No. 1.5;
0; Mismatches 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 257/3; 278/3; 309/3; 363/3; 424/1; 479/1; 501/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----KQAARGTSEPVGECTKKKKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T16K5
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106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                683/2;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                749/3; 808/3;
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17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proline-rich protein F7K2.50 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-Aug-1999
C;Accession: T05441
R;Bevan, M.; Wedler, H.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F
submitted to the Protein Sequence Database, November 1998
                                   A;Cross-references: GB:NC_001268; NID:g7269093; PIDN:CAB79202.1; C;Genetics:
                                                                                                                                  A;Title: Sequence and analysis of chromosome 4 of A;Reference number: A85001; MUID:20083488 A;Accession: D85257
                                                                                                                                                                                               extensin-like protein [imported] - Arabidopsis thaliana (rouse-ear cress) c;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #tex C;Accession: D85257 R:anonymous. The European Union Arabidopsis Genome Sequence 402, 769-777, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-379 <BEV>
A; Cross-references: EMBL: AL033545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
T05441
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A; Gene: AT4g22470
A; Map position: 4
                                                                            A; Molecule type: DNA
A; Residues: 1-379 <S'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 4
A; Note: F7K2.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z15416
A; Accession: T05441
                                                                                                                    A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: cultivar Columbia; BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.9
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
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                                                                                                                                                                                                                                                                                                                                                                                                                         258 SGSPPKNASTPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPPQPA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 MSPPLDRDGGVTSPVSNGEPINTAIPFAPIYNPPTAPRPVTDDTLKEYVRKQIEYYFSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305 ARTASKYSAASQQVQRNRGNAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 PVNPTIWPLMPTVSGADSLPGPSSQAPQQFRQNGPAATAAPVESQPQASS-SKPQQP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536 NLQKDFFLRRKMGPEGYLPVALIASFPRVRSLTEDYSLILEALKDSTKVDMSPDGLQIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                       79 STSPPPVATTPPALPPKPLPPP--LSPPQTTPPPPPAITPPPPPA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ~-RQEFYLRRARRRKFAWKPVLQSISEMKPVMEFHTPM~-AYRDSG----SP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MESPL-----PNLSGEALS---PTA----TAKDEITQMILKSAARSELGMYVSK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFEHQLDPHQASILIQQAQQ-----HMASFAPFRP------PMPMLSPHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSRKVFDYH---SVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANPHAPPKLTAAQRKERGP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EEWEEFDNEISGGGGSAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----PKNASTPSLPGPKNISP-----PRQVSVPQRSSPPPKNVSPPPQPAFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydroxyproline-rich glycoprotein
                                                                                <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107; DB Pred. No. 1; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- LPRWEDIEAGDDNFDYMTLMEAQYSQYYGAPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schueabase, November 1998
                                                                                                                                                                                                                                                              16-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                     Genome Sequencing Consortium, The Cold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 379;
                                                                                                                                                                             the plant Arabidopsis thaliana
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Search completed: September 16, 2002, 00:44:16 Job time: 595 sec
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A; Map position: 1
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Gene: F7012.5
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                                                                                                                                             269 QEELQRKFLEAVEKREHERLVREESWR-----VQEIARINREHEILAQERSMSAAKDAAV
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                                                                                                                                                                                                                                                                                                          140 -----PEPHLAGDRPSKHLKLVF-----IRHCLRALRLPRISIDLMESPL 179
                                                                                                               268 PSL-----PGPKNISPPRQVS----VPQRSSPPPKNVSPPPQP 301
                                                                                                                                                                            217 ROEF---YLRRARRR-----RKFAWKPVLQSISEMKPVMEFHTPMAYRDSGSPPKNAST 267
                                                                                                                                                                                                              213 PNISGDFLSDNSTS----SSSSYSTSSDMEMGGGTATTRKKRKRKWKVFFERLMKQVVDK 268
                                                                                                                                                                                                                                                                             153 SLHHHQQQTPLRPQQNNNNNNNNNNNSSIFSTPPPVTTVMPTLPSSSIPPVTQQINVPSF 212
                                                                                                                                                                                                                                                                                                                                             97 KMAEHGY----IRNAKKCKEKFENVYKYHKRTKEGRTGKSEGKTYRFFDQLEALESQSTT 152
                                                                                                                                                                                                                                                                                                                                                                          97 RFSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQ------QLESIRNEG-- 139
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Match Length
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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APC_MOUSE
DYN1_CAEELL
ZAP3_HUMAN
APC_HUMAN
APC_HUMAN
APC_HUMAN
APC_HUMAN
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APC_HUMAN
WS14_MOUSE
RW1_DROME
RW1_DROME
FXM1_DROME
FXM1_RAT
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MK07_MOUSE
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p22987 schizosacch
Q28062 bos taurus
Q10136 schizosacch
Q610136 schizosacch
Q61315 mus musculu
p39055 caenorhabdi
p49750 homo sapien
Q15911 homo sapien
Q15911 homo sapien
Q959m23 mus musculu
p13983 nicotiana t
p81322 mus musculu
Q9V7h4 drosophila
Q99V7h drosophila
Q99p31 mus musculu
Q99V7h mus musculu
Q99V696 mus musculu
Q99F091 rattus norv
Q61329 mus musculu
Q99F091 rattus norv
p46582 caenorhabdi
Q9ukn7 homo sapien
Q9wvs8 mus musculu
Q9yF085 homo sapien
Q9av87 mus musculu
Q9yF085 homo sapien
Q14687 homo sapien
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Q14687 homo sapien
Q99G18 drosophila
Q99G18 drosophila
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## LIGNMENT

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28062;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
                                                                                                                       aggrecan/versican family.";
J. BLOI. Chem. 269:10119-10126(1994).
-I- FUNCTION: MAY PLAY A ROLE IN THE TERMINALLY DIFFERENTIATING AND THE ADULT NERVOUS SYSTEM DURING POSTNATAL DEVELOPMENT. COULD STABILIZE INTERACTIONS BETWEEN HA AND BRAIN PROTEOGLYCANS.
-I- SUBCELLULAR LOCATION: SECRETED; EXTRACELLULAR MATRIX (BY
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                        Brevican core
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOVIN
                                                                                               +
                                                                                                                                                                                                                                   MEDLINE-94193597; PubMed-8144512;
                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                       Yamada H., Watanabe
                                                                                                                                                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                  "Molecular cloning of brevican, a novel brain proteoglycan aggrecan/versican family.";
                                                                                                                                                                                                                                                                                        NCBI_TaxID-9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 VVYPDGHVEN--LSKSCSVHDLLLGNPDYY------VCGSTPYTTTNRMAAE-----
           SIMILARITY).
TISSUE SPECIFICITY: BRAIN; EXPRESSED IN CER
NOT IN NEURONS.
NOT IN NEURONS.
PTM: CONTAINS MOSTLY CHONDROITIN SULFATE.
SIMILARITY: CONTAINS 1 IMMUNOCLOBULIN-LIKE
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY
                                                                                                                                                                                                                                                                                                                                               taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPGPKNISPPROVSVPORSSPPPKNVSPPPOPAFVARTASKYSAASQQVQRNRGNAK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRARRRKFAWKPVLQSISEMKPVMEFHTPM------AYRDSGSPPKNASTP--S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSRMLVTDPLKRATLEEVLNHPWMIRNYEGPPASFAPERSP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQSRKVFD-YHSVTMQQLES----IRN-EGPEPHLAGDRPSKHLKLVFIRHCLRALRLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP----SSPVQ-----PTSYNRTLPPMPEVV---AYKGDEESPRVSRNTSLAR 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRIRHAAHDIENPILPSLSMNTDIYDAFHPLISIYYLVSERRVYEKGGNWNRIAKTPVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLPLDPETTREMNGFDFGPPEKTVRELTKVISSEAYQSLAKTGFYSGPNSADKKKSFFE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           891
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66 266
154
1 141
247
620
778
98748 MW;
                                                                                                                                                                                                                                                                                                                                                                        protein precursor.
                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.7%;
21.8%;
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ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
V -> D (IN REF. 1).
V -> E (IN REF. 1).
I -> NL (IN REF. 1).
IR -> ML (IN REF. 1).
MW; 89D9BB6D825C0358 CRC64;
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Pred. No. 0
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                 FAMILY DOMAIN
                                                                                               IN CEREBELLAR
                                                           V-TYPE DOMAIN
                                                                                               ASTROCYTES
                                                                                                                                                                                                                                                                                                                    Bovoidea;
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В 8

368

140 PEPHLAGDRPSKHLKLVFIRHCLRALRLPR-----ISIDLME-----SPLPNLS 183 PASHLASDALE---AIVTVTETLEELKLPQEAVESESRGAIYSIPIIEDGGGGSSTPEDP 424

1 Similarity 54; Conser

Conservative

26;

101;

Indels

42;

Gaps

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SMART; SM00445; LINK; 2.

SMART; SM00445; LINK; 2.

A PROSITE; PS00022; EGF_1; 1.

R PROSITE; PS00186; EGF_2; 1.

R PROSITE; PS00299; IG_MHC; 1.

DR PROSITE; PS0061; C_TYPE_LECTIN_1; 1.

DR PROSITE; PS0061; C_TYPE_LECTIN_2; 1.

DR PROSITE; PS00041; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pfam; pF000uv, ...
pfam; pF00047; ig; 1.
pfam; pF00059; lectin_c; 1.
pfam; pF00059; xlink; 2.
pfam; pF000193; xlink; 2.
proDom; pF000193; Link; 2.
proDom; pF000318; Link; 2.
proDom; sM00032; CCP; 1.
R SMART; SM00034; CLECT; 1.
SMART; SM000181; EGF; 1.
SMART; SM00181; EGF; 1.
Query Match
Best Local S
Matches 54
                                                                                                                              DISULFID
CARBOHYD
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DOMAIN
DOMAIN
DOMAIN
DOMAIN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR000538; Link.
InterPro; IPR000436; Sushi_SCR_CCP.
InterPro; IPR001304; lectin_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X75887; CAA53481.1; -. HSSP; P20693; 1HLJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as 1 modified and this statement is not rementities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: CONTAINS 1 SUSHI (SCR) DOMAIN.
-!- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000561; EGF-like.
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SM00406;
SM00445;
                                                                                          6.7%;
                                                                                                      BY SIMILARITY.
BY SIM
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Score 116; DB
Pred. No. 0.37
26; Mismatches
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C-TYPE LECTIN.
SUSHI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BREVICAN CORE PROTEIN.
IG-LIKE V-TYPE DOMAIN.
LINK 1.
LINK 2.
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                       DB 1;
.37;
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                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                       Matches
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Q10136;
Q1-FEB-1996
Q1-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ste7 protein.
STE7 OR SPAC23E2.03C.
SCh1zosaccharomyces pombe (Fission yeast).
Sch1zosaccharomycetes;
Eukaryota; Fung1; Ascomycota; Sch1zosaccharomycetes;
Eukaryota; Fung1; Ascomycota; Sch1zosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: HAS A ROLE IN PROMOTING MEIOSIS WHEREBY IT IS INVOLVED IN ESTABLISHING THE MATING PHEROMONE SIGNALING PATHWAY. IT ALSO HAS A ROLE IN SUPRESSING MEIOSIS UNTIL THE CONJUGATION PROCESS IS COMPLETE.
-!- INDUCTION: BY NITROGEN STARVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND CHARACTERIZATION.
MEDLLINE=20296734; PubMed=10835379;
Matsuyama A., Yabana N., Watanabe Y., Yamamoto M.;
"Schizosaccharomyces pombe Ste7p is required for both promotion withholding of the entry to meiosis.";
Genetics 155:539-549(2000).
                                                                                                                                                                                                                                                                                                                                                                                                 Conjugation; Meiosis; Pheromone.
DOMAIN 200 261 SER
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                           Local
                                                        SVTMQQLESIRNEGPEPHLAGDRPSKHL----
                                                                                                                                                      VTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGV-HVRELRSPTHGSQQSRKVFDYH 125
EAT----EIFTHSQPLPIPAGPSSKSHAIDFKFKFPSKSASSLPCSKSNDSMVNICYMLK 125
                                                                                                              ITGKICFETNA - -
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                                                                                                                                                                                                                                        Similarity
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464
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(Rel.
(Rel.
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40,
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61101 MW;
                                                                                                                                                                                                                                  6.5%;
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Last sequence up
Last annotation
                                                                                                                                                                                                                 35;
                                                                                                                                                                                                            Score 112.5; DE
Pred. No. 0.37;
35; Mismatches 1
                                                                                                                                                                                                                                                                                                                                           SER-RICH.
SER-RICH.
; FDD23893E9A7A6AC CRC64;
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                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                              120;
                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                              Indels
                                                ---KLVFIRHCLR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walsh
                                                                                                                                                                                                            85;
                                                                                                                                                                                                            Gaps
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                                              ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY SIMILARITY).

SIMULATION STAI SUBURIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY SIMILARITY).

-i- SUBURIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS (BY SIMILARITY).

-i- ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; PRODUCED BY ALTERNATIVE SPLICING.

-i- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART, LUNG, BRAIN, STOMACH, INVESTIME, TESTIS AND OVARY.

-i- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).

-i- SIMILARITY: CONTAINS 7 ARM REDEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APC_MOUSE S
Q61315; Q62044;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
16-OCT-2001 (Rel
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                                                                                                                                                                                                                          Oshima M., Sugiyama H., Kitagawa K., Taketo M.;

"APC gene messenger RNA: novel isoforms that lack exon 7.";

Cancer Res. 53:5589-5591(1993).

-i- FUNCTION: TUMOR SUPPRESSOR, ALLOWS THE RAPID TURNOVER OF BETA-
CATEMIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-45 FROM N.A.
STRAINB/C; TISSUB-Liver;
Dicker F., Lambertz S., Reitmair A., Ballhausen W
The murine APC gene: alternative splicing of 5'
region segments.";
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STRAIN-GOTORMS 1 AND 2),
STRAIN-GOTORMS, AND CAST/EI; TISSUE-BR
MEDLINE-92263101; Pubmed-1350108;
Su L.-K., Kinzler K.W., Vogelstein B.,
Luongo C., Gould K.A., Dove W.F.;
"Multiple intestinal neoplasia caused benould of the APC gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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colyposis coli protein (APC pro
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Sciurognathi; Muridae;
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EMBL; U02997; AAA03443.1; -.
HSSP; Q02248; 3BCT.
MGD; MGI:88039; Apc.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 6.
SMART; SM00185; ARM, 5.
PROSITE; PS50176; ARM_REPEAT; 1.
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                                                                                                                                                                             SAASQOVQRNRGNAKSLY 329
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Dynamin (EC
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STRAIN-BRISTOL N2;
MEDLINE-97439883; PubMed-9294229;
                                                                                                                                                                                                                                                                                                                                           Pfam, PF00350; dynamin; 1.
pfam, PF01031; dynamin_2; 1.
pfam, PF02212; GED; 1.
pfam, PF00169; PH; 1.
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Rhabditidae; Pelode
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                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L29031; AAB72228.2; -. HSSP; Q05193; 2DYN. InterPro; IPR001401; Dynamin InterPro; IPR000375; Dynamin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                         SMART; SM00053; DYNC; 1.
SMART; SM00302; GED; 1.
SMART; SM00233; PH; 1.
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InterPro; IPR001849;
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                                                                                                                                                                                                                                  Endocytosis.
                                                                                                                                                                                                                                                Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTP. MOST PROBABLY INVOLVED IN VESICULAR TRAFFICK PARTICULAR RENDOCYTOSIS.

PARTICULAR ENDOCYTOSIS.

CATALYTIC ACTIVITY: GTP + H(2)0 = GDP + phosphate.
SUBCELULAR LOCATION: MICROTUBULE-ASSOCIATED.
SIMILARITY: BELONGS TO THE DYNAMIN FAMILY.

SIMILARITY: CONTAINS 1 PH DOMAIN.
IRHCLRALR--LPRISIDLMESPLPNLSGEALSPTATAKDEITQMILK----SAARSELG
                            FLRAGVYPEKQKAQEDESQQEMEDTSIDPQLERQVETIRN------LVDSY
                                                     FSKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVF 157
                                                                                                  Similarity
                                                                                                                                                                                                                                                             PS00410; DYNAMIN; 1
PS50003; PH_DOMAIN;
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                                                                                                                                                                                                                                                Motor
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207
519
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                                                                                    Conservative
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                                                                                                                                                                                                                                               protein; GTP-binding; Microtubules; Multigene family;
                                                                                                                                                          47 G
142 G
210 G
624 F
93348 MW;
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
PH.
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P49750; P49752; (
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16-OCT-2001 (Rel
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Nature 375:754-760(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Levesque Ikeda M., Chi H., Lin C., Li G., Holman K., TSuda T., War L., Foncin J.-F., Bruni A.C., Wontesi M.P., Sorbi S., Rainero I., Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Polinsky R.J., Wasco W., da Silva H.A.R., Haines Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;
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Rowen L., Madan A.
Bloom S., Dors M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rowen L., Madan A., Qin S., Abbasi N., Baradarani L., Birditt Bloom S., Dors M., Dickhoff R., Fleetwood P., Harrison G., Jan Kaur A., Madan A., Owen M.P., Ratcliffe A., Shaffer T., Hood I "Sequencing of human chromosome 14024.3 region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF
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                                                                                                                                                                                                                                                                                 send an
                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Nuclear (Potential). CAUTION: Ref.2 sequence differs from that shown frameshift in position 1661.
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L40403; AAC42008.1; AI
L40400; AAC42006.1; -
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requires a license agreement (See lan email to license@isb-sib.ch).
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Query Match

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STANDARD;

PRT; 2843

P25054; Q15162; Q15163;

P 01-MAY-1992 (Rel. 22, Created)

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T 16-CCT-2001 (Rel. 40, Last annotation upda

E Adenomatous polyposis coll protein (APC
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VARIANTS FAP.

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VARIATINE-9135211; PubMed-1651563;

NIShisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A.,

Nishisho I., Nakamura Y., Baba S., Hedge P., Markham A., Krush A.J.,

Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,

Royama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,

Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,

Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,

Pereisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;
                                                                                                                                                                                                                                                                                               Nagase H., Nakamura Y.; "Mutations of the APC (adenomatous Hum. Mutat. 2:425-434(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASSOCIATION WITH CATENINS.

MEDLINE=94082395; PubMed=8259519;
Su L.-K., Vogelstein B., Kinzler K.W.;

"Association of the APC tumor suppress;
Science 262:1734-1737(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uslyn G., Carlson M., Thliveris A., Albertsen H., Gelber Samowitz W., Groden J., Stevens J., Spirio L., Robertson Sargeant L., Krapcho K., Wolff E., Butt R., Hughes J.P., Warrington J., McPherson J.D., Wasmuth J., Le Paslier D., Abderrahim H., Cohen D., Leppert M., White R., "Identification of Annation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of deletion familial polyposis locus."; Cell 66:601-613(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94154728;
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MEDLINE=91335210; PubMed=1651562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=1678319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.1%;
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Stella A., Montera M., Resta N., Marchese C., Susca F.,
Romio L., Pilia S., Prete F., Mareni C., Guanti G.;
"Four novel mutations of the APC (adenomatous polyposis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Romio L.,
Hum. Mol.
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Nakamura Y., Horii A.;
"Somatic mutation of t
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Nakatsuru S., Yanagisawa A., Ichii
                                           Redston M., Nathanson K.L., Yuan Z.Q., Neuhausen S.L., Satagopan Wong N., Yang D., Nafa D., Abrahamson J., Ozcelik H., Antin-Ozerkis D., Andrulis I., Daly M., Pinsky L., Schrag D., Gallinger S., Kaback M., King M.-C., Woodage T., Brody L.C., Godwin A., Warner E., Weber B., Foulkes W., Offit K.; "The APC I1307K allele and breast cancer risk."; Nat. Genet. 20:13-14(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stella A.,
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VARIANT FAP W-1348,
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                                                                                                                                                                                                                           VARIANT LYS-1307.
MEDLINE-98400248; PubMed-9731522;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97144176; PubMed-8990002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT FAP ILE-171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eening for germ-line mutations in familial adenomatous polyposis
ents: 61 new patients and a summary of 150 unrelated patients.";
Mutat. 1:467-473(1992).
                                                                                                                                                                                                                                                                                                       Mutat.
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s in very well differentiated
LYS-1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Montera M., Resta N., Marchese Pilla S., Prete F., Mareni C., (Genet. 3:1918-1918(1994).
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                                                                                                                                                                                                                                                                                                       9:7-16(1997).
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AND
GLN-1317
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Guanti G.;
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NAT. MOG. 5:10/1-10/2 (1999).

1-1-FUNCTION: TUNOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETACATION: TUNOR SUPPRESSOR. ALLOWS THE PROSPHORYLATION STATE ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN.

1-1-ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SSOCIATES WITH CATENINS.

1-1-ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

1-1-PTM: PHOSPHORYLATED BY GSK-3B.

1-1-PTM: PHOSPHORYLATED GSK-3B.

1-1-PTM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wallis Y.L., Morton D.G., McKeown C.M., Macdonald F.; "Molecular analysis of the APC gene in 205 families: extended genotype-phenotype correlations in FAP and evidence for the roapc amino acid changes in colorectal cancer predisposition."; Med. Genet. 36:14-20(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Frayling I.M., Beck N.E., Ilyas M., Dove-Edwin I., Goodm Pack K., Bell J.A., Williams C.B., Hodgson S.V., Thomas Talbot I.C., Bodmer W.F., Tomlinson I.P.M.;
"The APC variants Il307K and El317Q are associated with tumors, but not always with a family history.";
Proc. Natl. Acad. Sci. U.S.A. 95:10722-10727(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The type of somatic mutation at APC in familial adenomatous polyposis is determined by the site of the germline mutation: a new facet to Knudson's 'two-hit' hypothesis."; Nat. Med. 5:1071-1075(1999).

-I- FUNCTION: TUMOR SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99401091; PubMed-10470088;
Lamlum H., Ilyas M., Rowan A., Clark S.,
Frayling I.M., Efstathiou J., Pack K., Pa
Gorman P., Sheer D., Neale K., Phillips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99138651; PubMed=9973276;
Gryfe R., Di Nicola N., Lal G., Gallinger S.,
"Inherited colorectal polyposis and cancer ris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT FAP PRO-1184
MEDLINE-99401091; Pu
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MEDLINE=99138651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The APC I1307K allele and Ashkenazi Jews.";
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MEDLINE-98400259; PubMed-9731533;
Woodage T., King S.M., Wacholder S.,
McAdams M., Laken S.J., Tucker M.A.,
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MEDLINE-98393712; PubMed-9724771;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99133859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS FAP CYS-1171 AND THR-2738, AND VARIANTS GLY-1057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hum. Genet. 64:378-384(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9950360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linger S., Redston M.;
cancer risk of the APC I1307K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ., Johnson V., Bell
Payne S., Roylance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R., Talbot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         community-based study
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., Thomas H.J.W.,
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015911; 013719; 015101;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Alpha-fetoprotein enhancer binding protein (AT motif-binding factor)
(AT-binding transcription factor 1).
                                                                                                                              MEDILINE-99425270; PubMed-10493829; """
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA shuman chromosome 16p and 16q.";
                                                                                                                                                                                                                                                                                                                                                MO1. Cell. Biol. 11:6041-6049(1991).
[3]
SEQUENCE OF 1-1190 FROM N.A. (ISOFORM A).
                                                                                                                                                                                                                                                                                                                                                                                                            MEDIINE-92049333; PubMed-1719379;
MORINAGA T., Yasuda H., Higashio K., Tamaoki T.;
"A human alpha-fetoprotein enhancer-binding protein, ATBF1, contains four homeodomains and seventeen zinc fingers.";
MOI. Cell. Biol. 11:6041-6049(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                              SEQUENCE OF 1151-3703 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization of an ATBF1 isoform that expresses neuronal differentiation-dependent manner."; neuronal differentiation-dependent manner."; neuronal differentiation-dependent manner.";
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DATABASE: NAME-APC; NOTE=Information about APC mutations;
WWWW="http://perso.curie.fr/Thierry.Soussi/APC.html".
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             McQuerry Y., Hotic M.;
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|-----GAKPSVK--SELSPVAR-QTSQIGG
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         PARTE 
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SMART; SM00389; HOX; 4.

SMART; SM00355; ZnF_C2H2; 21.

SMART; SM00451; ZnF_U1; 7.

PROSITE; PS00027; HOMEDBOX_1; 2.

R PROSITE; PS50171; HOMEDBOX_2; 4.

R PROSITE; PS50157; ZINC_FINGER_C2H2_1; 14

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 9.
                          Alternative

ZN_FING

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EMBL; D10250; BAA01095.1; -.
EMBL; AC002044; AAC31674.1; -.
EMBL; AC004943; AAC79153.1; -.
HSSP; P06601; 1FJL.
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-!- FUNCTION: Transcriptional activator that binds to the AT
sequence of the enhancer element of the AFP gene.
-!- SUBCELLULAR LOCATION: Nuclear.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B;
produced by alternative splicing.
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726 750
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IPR003604;
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                                                                                         C2H2-TYPE.
POLY-PRO.
POLY-GLU.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-GLN.
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HOMEOBOX 4
C2H2-TYPE.
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Best Local S
Matches 44
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MUS musculus (Mouse).

Eukaryota; Metazoa; Chordata; C

Mammalia; Eutheria; Rodentia; S

NCBI_TaxID=10090;
[1]
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DOMAIN
                                                                                                                                                             SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDILING-21153101; PubMed-11230181;
Cairo S., Merla G., Urbinati F., Ballabio A., Reymond A.;
Cairo S., Merla G., Urbinati F., Ballabio A., Reymond A.;
"MBSCR14, a gene mapping to the Williams-Beuren syndrome deleted
region, is a new member of the Mix transcription factor network.
Hum. Mol. Genet. 10:617-627(2001).
-I- FUNCTION: TRANSCRIPTIONAL REPRESSOR. BINDS TO THE CANONICAL
NON-CANONICAL E BOX SEQUENCES 5'-CACGTG-3' (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WS14_MOUSE STANDARD: PRT; 864 AA. 099MZ3; Q99MZ0; Q99MZ1; Q99MZ2; Q99MZ9; Q1-MAR-2002 (Rel. 41, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Williams-Beuren syndrome chromosome region 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _MOUSE
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                                                            SIMILARITY).
SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).
SUBCELULAR LOCATION: NUCLEAR (BY SIMILARITY).
ALTERNATIVE PRODUCTS: 5 ISOFORMS; 1/ZETA (SHOWN HERE), 2/THETA,
ALTERNATIVE PRODUCTS: 5 RE PRODUCED BY ALTERNATIVE SPLICING
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                          TRANSCRIPTION FACTORS. BHLH-ZIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KNASTPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLVSLPSLPQPPPQAPPPQCPLPQ-SSPSPSQLSHLP 2508
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A -> S (IN REF. 3).

A -> P (IN REF. 3).

T -> A (IN REF. 3).

I -> V (IN REF. 3).

A -> V (IN REF. 3).

A -> V (IN REF. 3).

A -> S (IN REF. 3).

A -> GEWSHRHGRERGLGVHLLETSRGLLFEGDVTDPAGPH

VOV (IN REF. 3).
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Pred. No. 20;
20; Mismatches
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MISSING.
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G -> GGG.
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Sciurognathi; Muridae;
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0F62AF37D4DCF856 CRC64;
                                             SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                      Muridae;
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; Murinae; Mus
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Matches 44
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EMBL; AF245476; AAK20941.1; --
EMBL; AF245477; AAK20942.1; --
EMBL; AF245478; AAK20943.1; --
EMBL; AF245478; AAK20944.1; --
EMBL; AF245479; AAK20944.1; --
HSSP; P25912; 1HLO.
MGD; MGJ:1927999; WBDSCT14.
InterPro; IPR003015; HLH_dim.
InterPro; IPR003015; HLH_Myc.
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Alternative splicing.
DOMAIN 345 350
DNA_BIND 660 674
DOMAIN 700 714
DOMAIN 715 736
VARSPLIC 545 556
                                                                                                                                                                                                                                                                                                                                            LT 10
LTOBAC
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SEQUENCE
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VARSPLIC
                                       Nicotiana tabacum (Common tobacco).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4097;
                                                                                                                                                                                     EXTN_TOBAC STANDARD; PRT; 620 AA. p13983; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Extensin precursor (Cell wall hydroxyproline-rich
                                                                                                                                                                     HRGPNT3.
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SMART; SM00353; HLH;
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPVPFSVDHLPHGYLEPVFGPH----FTVPQGMQPRCKPSSPSPGGQKASPPTLASATAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS00038; HELIX_LOOP_HELIX; 1.
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864
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699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK20940.1; -...
AAK20941.1; -...
AAK20942.1; -...
AAK20943.1; -...
AAK20944.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>Α</u>
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94874 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      864
714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 102.5; E
Pred. No. 3.5;
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IN ISOFORM 4).
MISSING (IN ISOFORM 4)
; 7E6AFFB04C71B327 CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSKATTLQKTAEVILMLQQERAAMQEEAQQLRDBIEELNAA
INLCO -> GLPTQRPTLVALAGEQSNHASEDSGVHPDAAA
GTGSYAGGGAAAAG (IN ISOFORM 3).
MISSING (IN ISOFORM 3).
VSKATTLQKTAEVILM -> LPGLANTEAHIGGARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEUCINE-ZIPPER.
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASIC DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN ISOFORM 2).
AKPEQALEPPTM -> VVLIVLPVPSQA (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELIX-LOOP-HELIX MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
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C outstation -
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us-09-828-313-35.rsp

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RESULT
IRS2_M
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Best Local
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regulares a license agreement (See http://www.isb-sib.ch/announce/
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLLINE-95405472; PUBMed-7675087;
Sun X.J., Mang L.-M., Zhang Y., Yenush L., Myers M.G. Jr.,
Glasheen E., Lane W.S., Pierce J.H., White M.F.;
"Role of IRS-2 in insulin and cytokine signalling.";
Nature 377:173-177(1995).
-i- FUNCTION: MAY MEDIATE THE CONTROL OF VARIOUS CELLULAR PROCESSES
BY INSULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X13885; CAA32090.1; -. PIR; S06733; S06733. Repeat; Cell wall; Glycoprot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keller B., Lamb C.J.; "Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation."; Genes Dev. 3:1639-1646(1989).
-i- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV XANTHI;
MEDLINE=90128263;
                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
Insulin receptor substrate-2 (IRS-2) (4PS).
                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     IRS2_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: EXTENSINS CONTAIN A CHARACTERISTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Extracellular matrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SER-PRO(4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNVSPPPQPAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPSFSPPPPTYEQSPPPPPAYSPPLPAPPTYSPPPPTYSPPPTYAQPPPLPPTYSPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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151
242
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65406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal;
                                                                                                                                                                                       Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
EXTENSIN.
H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
1.
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3 X APPROXIMATE TANDEM REPEATS.

641DD2278AB28524 CRC64;
                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                     1321
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; Murinae; Mus
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Best Local S
Matches 78
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SMART; SM00310; PTBI;
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-!- SIMILARITY: CONTAINS
-!- SIMILARITY: CONTAINS
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InterPro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: SKELETAL MUSCLE,
                                                                                                               549
                                                                                                                                                                                                                               396
719 YKASS
                 311
                                     659
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                                                                         603
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                                                                                                                                                                                          439
                                                                                                                                                                                                           87 VVHRGSKILPRFSKHG-------VHVRELRSPTHGSQQS------
                                                                                                                                                                                                                                                 27 LSKSCSVHDLLLGNPDYYVCGSTPYTITNRMAAEEVLEYGVTYFVCATPNAQPFLERQPK 86
                                                                                                                                                                    VFDYHSV--TMQQLESIRNEGPEP-------HLAGDRPSKHLKLVFIRHC 161
                 YSAAS
                                                                                                                                                                                         ATSPGS--LSSSSGHGSGSYPLPPGSHPHLPHPLHHPQGQRPSSGSASASGSPSDPGFMS 496
                                     RSGGPNSCKSDDYMPMSPTSVSAPKQILQPRLAAALPPSGAAVPAPPSGVGRTFPVNGGG
                                                      DSGSPPKNASTPSLP-GPKNISPPRQVSVPQRSSP-PPKNVSPPPQPAFVART----ASK
                                                                         GSSGRLCPSFPASSPKVAYNPYPEDYGDIEIGSHKSSSSNLGADDGYMPM---
                                                                                            LRRAR-----RRRKFAWKPVLQSISEMK----
                                                                                                              GRPYR--RVSGDGAQDLDRGLRKRTYSLTTPAR----QRQVPQPSSASLDEYTLMRATFS
                                                                                                                                LRALRLPRISIDLMESPLPNLSGEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFY
                                                                                                                                                    LDEYGSSPGDLRAFSSHRSNTPESIAETPPARDGSGGELYGYMSMDRP--
                                                                                                                                                                                                                              LSRS---HTLSAG-----CGGRPSKVT-LAPAGGALQH-----SRSNSMPVAHSPPA 438
                                                                                                                                                                                                                                                                     78;
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78; Conservative
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                                                                                                                                                                                                                                                                    43;
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                                                                                                                                                                                                                                                                  Score 101.5;
Pred. No. 7;
13; Mismatches
                                                                                                                                                                                                                                                                                                                   WW;
                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION
(BY SIMILARITY).
POLY-ASN.
POLY-SER.
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PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                   5069CE9D614960C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LUNG, BRAIN, LIVER, KIDNEY,
                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                    131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INSR)
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                      Length 1321;
                                                                                            -PVMEFHTPMAYR 256
                                                                                                                                                                                                                                                                    113;
                                                                                                                                                    ----LSHC
                                                                         TPGAAL
                                                                                                                                                                                                            -RK 120
                                                                                                                                                                                                                                                                    Gaps
                                                       310
                                                                         658
                                                                                                               602
                                                                                                                                  221
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Berondon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Berandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Dayle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dablike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dablike C., Davenport L.B., Davies P.,
RA de pablos B., Delchar A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA deloke R., Gong F., Gorrell J.H., Gu Z., Gunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibeywam C.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Morris J., Lia Z.,
RA McMulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Ralnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Y., Wassarman D.A., Weinstock G.M., Diang S., Zhao Q., Zheng L.,
RThe genome sequence of Drosophila melanogaster.";

RC 1. Schence 28:2185-2195(2000).
Matches
            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RW1_DROME
09V7H4;
16-OCT-2001
16-OCT-2001
16-OCT-2001
RW1_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG8370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                            FlyBase; FBgn0034060; CG8370.
InterPro; IPR011121; G_adapt_C.
Pfam: PF02883; Alpha_adaptinC2;
SEQUENCE 1540 AA; 170274 MW;
                                                                                                                                                                      EMBL; AE003808; AAF58081.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 40,
(Rel. 40,
(Rel. 40,
Conservative
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
39;
                Score 101; DB 1; Length 1540; Pred. No. 9.2;
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                                                                           1.
; 5A8C97531D425846 CRC64;
    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brachycera; Muscomorpha;
    71;
    108;
    Gaps
    10;
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RESULT 13
PC15_MA
AC 099PJI
AC 099PJI
DT 01-MAA
DT 01-MAA
DT 01-MAA
DT 01-MAA
DT 01-MAA
DT 01-MAA
DT 10-MAA
DT 10-MA
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murcha C.L., Woychik R.P.;
Murcha C.L., Woychik R.P.;
Expression of Podh15 in the inner ear, nervous system epithelia of the developing embryo.";
epithelia of the developing embryo.";
Mech. Dev. 105:163-166(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1234
                                                                                                                                                                                                                                                                           embryonic day 16.

- IDISEASE: Defects in PCDH15 are the cause of the Ames waltzer (av) phenotype. It is characterized by deafness and a balance disorder. associated with the degeneration of inner ear neuroepithelia.
- i- SIMILARITY: CONTAINS 11 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woychik R.P.;
"The mouse Ames waltzer hearing-loss mutant is caused by mutation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCDH15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protocadherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PC15_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=11429292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20578757;
Alagramam K.N., Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
TISSUE SPECIFICITY: Expressed in brain and sensory epithellum the developing inner ear. Also found in the spleen, developing eye, dorsal root ganglion, dorsal aspect of neural tube, floor plate and ependymal cells adjacent to the neural canal.
DEVELOPMENTAL STAGE: Highest level of expression is detected at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: Calcium-dependent cell-adhesion F maintenance of normal retinal and cochlear inner ear neuroepithelial cell elaboration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VFDYHSVTMQQ--LESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRISIDLMESP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PNKPPEQRVLKEQNGSAKKMGKTPGRER 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPQGVPISVQVRPQKKVKPTPAVVLGTTKPKQEVSTPVADQHEKSLAKSSPPQQENISPK 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLPG------QRSSPP-PKNVSPP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSKSSWSPWSMDMNALSKHLQKAKPKTVVSTPVTPPAASAPAAAPVPLPEAKPVKKSSTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a novel protocadherin net. 27:99-102(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=11138007;
urcia C.L., Kwon H.Y., Pawlowski K.S., Wright C.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
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Best Local
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DOMAIN
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CARBOHYD
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DOMAIN
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PROSITE; PS50266; CADHERIN_2; 11.
Cell adhesion; Glycoprotein; Transmembrane; Calcium-binding; Signal; Multigene family; Vision.
                                                                                                                                             1711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00205; CA; SMART; SM00112; CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002126; Cad
Pfam; PF00028; cadherin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF281899;
HSSP; P09803; 19
1784 SLPISTPPTSSLPLPPPLSLPPPPRP 1809
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                                                                                                                                                                                    166
                                    281
                                                                                                           226
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                                                                                                                                                                                                                    EQLKSLSSGSSFSSSWSHFSFSTLPTISRAVELGSEPNVVTSPADCTLEL-----SPPL
                                                                                                                                                                                                                                                    RELRSPTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRAL 165
                                                                                                                                                                                                                                                                                           WQITNQRAECESARCHPSQRGSSNVLLATEDAH---ESEKEGGHRDTLIVQQ------ 1656
                                                                                                                                                                                                                                                                                                                           YTITNRMAAEEVL-----EYGVTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGVHV 105
                                    --QVSVPQRSS---PPPKNVSPPPQP
                                                                        PKRNSFEIAPHPPSIFAPLP----HPPLP----
                                                                                                         RRRRKFAWKPVLQSISEMKPVMEFHTPMAYRDSGSPPKNASTPSLP-GPKNISPPR----
                                                                                                                                               R-PRI------LNSLSSKRETPTCASDTE-
                                                                                                                                                                                RLPRISIDLMESPLPNLSGEALSPTATAKDEITQMILKSAARSELGMYVSKRQEFYLRRA
                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1804
57
102
204
424
567
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1069
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1437
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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23.7%;
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 7.
CADHERIN 7.
CADHERIN 9.
CADHERIN 9.
CADHERIN 10.
CADHERIN 11.
                                                                                                                                                                                                                                                                                                                                                                                  Score 100; I
Pred. No. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTOCADHERIN 15.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           E3D7DB9F5F738652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GLCNAC. .
                                                                        -RPPIAFTTFPLPLSPPNPPPPQLVTF 1783
                                                                                                                                                                                                                                                                                                                                                                                                    DВ
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                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                    1710
                                                                                                           280
                                                                                                                                                                                225
                                                                                                                                             1732
                                                                                                                                                                                                                                                                                                                                                                12;
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RESULT 14 APC\_RAT

Query Match Best Local Similarity

5.8%;

Score 100; DB Pred. No. 23; 40; Mismatches

DB 1; Length 2842; 97;

Indels

74;

Gaps

12;

Matches

59;

Conservative

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APC_RAT
P70478;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 32.31 JAN. 12.37. - 1- FUNCTION: THOM SUPPRESSOR. ALLOWS THE RAPID TURNOVER OF BETA-CATENIN. APC ACTIVITY CORRELATED WITH ITS PHOSPHORYLATION STAT ALLOWS THE DOWN-REGULATION OF CYTOPLASMIC BETA-CATENIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINEFISCHER 344/N. TISSUE-Brain;
MEDLINE-96116966; PubMed-8563176;
TOyota M., Ushijima T., Kakluchi H., Watanabe M.,
Sugimura T., Nagao M.;
   DOMAIN
MUTAGEN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K., Weisburger J.H., Sugimura T., Nagao M.; "Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the Apc gene in rat colon tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine."; proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
                                                         DOMAIN
DOMAIN
                                                                                  DOMAIN
DOMAIN
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=SPRAGUE-DAWLEY, AND FISCHER 344/N; MEDLINE=95148647; PubMed=7846077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "cDNA cloning of the rat APC gene and Mamm. Genome 6:746-748(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>'</del>
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                                             DOMAIN
                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                  PROSITE; PS50176;
                                                                                                                                                                                                                                                 Pfam; PF00514; Armadillo_seg; 6 SMART; SM00185; ARM; 5.
                                                                                                                                                                                                                                                                                       EMBL; D38629; BAA07609.1; ... HSSP; Q02248; 3BCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
                                                                                                                                                                                                                                                                            [nterPro; IPR000225; Armadillo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
SUBUNIT: FORMS HOMOOLIGOMERS AND ASSOCIATES WITH CATENINS SIMILARITY).
    125
451
503
546
590
637
682
724
739
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1156
1864
2842
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
polyposis coli protein (APC protein).
                                                                                                                                                                                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
   ΑĄ,
                                                                                                                                                                                                                                   ARM_REPEAT; 1.
                                                          2831
1155
                                                                                                   493
545
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636
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723
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      310530
ARM 1.

ARM 2.

ARM 3.

ARM 4.

ARM 5.

ARM 5.

ARM 6.

ARM 7.

SER-RICH.

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (ACIDIC).

HIGHLY CHARGED.

HIGHLY CHARGED.

C->R: IN AN IO-INDUCED COLON TUMOR.

30 MW; 3CBB2EA8A34EBF47 CRC64;
                                                                                                                                                                             COILED COIL (POTENTIAL)
                                                                                                                                                                                                          LEU-RICH
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                                                                                                                                                                                                                    Coiled coil; Repeat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chromosome 18.";
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InterPro; IPR001356; Homeobox.

R InterPro; IPR003604; ZnF_U1.

R InterPro; IPR003604; Znf-C2H2.

R Pfam; PF00046; homeobox; 4.

R Pfam; PF00096; zf-C2H2; 20.

R SMART; SM00355; ZnF_C2H2; 22.

R SMART; SM00355; ZnF_U1; 7.

R SMART; SM00355; ZnF_U1; 7.

R PROSITE; PS00027; HOMEOBOX_1; 2.

R PROSITE; PS00028; ZINC_FINGER_C2H2_1; 15.

R PROSITE; PS00028; ZINC_FINGER_C2H2_2; 9.

R PROSITE; PS0157; ZINC_FINGER_C2H2_2; 9.

Transcription regulation; Activator; Zinc-finger; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABFI_MOUSE STANDARD; PRT; 3726 AA. 061329; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Alpha-fetoprotein enhancer binding protein (AT-binding transcription factor 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D26046; BAA05046.1; -. HSSP; P06601; 1FJL. MGD; MGI:99948; Atbf1.
                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99948; Atbf1.
Interpro; IPR001356; H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2341 KLSQLPRTSSPSTAST----KSSGSGKMSY 2366
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Job time: 458 sec
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

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56 RMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVHR-----GSKILPRFSKHGVHVRELR 109 : : : | : | | | : | : 42 MTPSNMAIVLG-PNLLWPQAEGNITEMMTTVSLQIVGIIEPIIQHADWFFPGEIEFNITG 100 3 LTPFSCVTVQGYVRVVYP--DGHVENLSKSCSVH-----DLLLGNPDYYVCGSTPYTITN 55 Query Match 7.6%; Score 131; DB 4; Length 413; Best Local Similarity 20.6%; Pred. No. 0.0017; Matches 78; Conservative 57; Mismatches 142; Indels 1

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ALIGNMENTS

## RESULT Q9Y4Q4 ID Q9Y Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL096728; CAB46376.1; HSSP; Q07960; 1RGP. InterPro; IPR000198; P\_rich\_extensn. InterPro; IPR000198; RhoGAP. PRINTS; PR01217; PRICHEXTENSN. SMART; SM00324; RhoGAP; 1. Hypothetical protein. HYPOTHER 1 AA; 43398 MW; 872B63B9DB4FC0EF CRC64; Q9Y4Q4 PRELIMINARY; PRT; 413 AA. Q9Y4Q4; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 43.4 KDA PROTEIN (FRAGMENT). Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI\_TaxID=9606; TISSUE=TESTIS; DKFZP434B034. SEQUENCE FROM N.A. s:

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01-NOV-1998;
01-NOV-1998;
01-JUN-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DNA Res. 5:169-176(1998).
EMBL; AB014572; BAA31647-1; -.
HSSP; Q07960; 1RGP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LPRISIDLMESPLPNLSGEALSP----TATAKDEITQMILKSAAR-------
                                                                                                                                                                                                                                                                                                               RMAAEEVLEYGVTYFVCATPNAQPFLERQPKVVHR-----GSKILPRFSKHGVHVRELR 109
                                                                              RHCLRALRLPRISIDLMESPLPNLSGEALSP----TATAKDEITQMILKSAAR-----
                                                                                                                                                                                               S-----PTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFI 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 20.7
80; Conservative
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(TrEMBLrel. 08, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
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                            -LPEQPLDSPAAPALSPSGLGLQPGPERTSTTKSK--ELSPGSAQKGSPGSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.3%; Score 126; DB 4; Length 818; 20.7%; Pred. No. 0.012; tive 55; Mismatches 140; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            996C8ECF9B523808 CRC64
                                                                                                                                         -SCAPPSMQPPAPPAELAAPLPSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 112;
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RX MEDILINE-20195005; PubMed-10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Pfelifer B.D.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Pfelifer B.D.,
RA George R.A., Lewis S.E., Richards S. Rahman Q., Chen L.X.,
RA George R.A., Lewis S.E., Richards S. R., Champe M., Pfelifer B.D.,
RA George R.A., Bayend J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Barchale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Buck J., Brokstein P., Brottler P.,
RA Ballew R.M., Basu A., Buck J., Barokstein P., Brottler P.,
RA Ballew R.M., Basu D.A., Butler H., Caddeu E., Center A., Chandra I.,
RA Bartis W.L., Beros P.V., Berman B.P., Bhandari D., Bolshakov S.M.,
RA George R.A., Bouck J., Berokstein P., Brottler P.,
RA George R.A., Bouck J., Berokstein P., Brittis M.,
RA Harris M.L., Harvey D., Dahlke C., Davenport L.B., Dew I., Dietz S.M.,
RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X.,
RA Merkilov G., Milshana N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshana N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshana N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkilov G., Milshana N.V., Mobarry C., Morris J., Woshrefi A.,
RA Merkilov G., Milshana N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mang E.Y., Massarman D.A., Meinstock G.M., Weissenbach J.,
RA Mang E.Y., Massarman D.A., Meinstock G.M., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
01-MAY-2000
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VZT8
EMBL; AE003477; AAF47729.1; -. HSSP; P56276; 1TLK. FlyBase; FBgn0035410; CG14964.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tremblrel 13, (Tremblrel 13, 13) (Tremblrel 13, 15)
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Last annotation update)
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Best Local 9
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09LQ09;
01-OCT-2000 (TrembLrel. 15, C
01-OCT-2000 (TrembLrel. 15, I
01-UN-2001 (TrembLrel. 17, I
P16P17.12 PROTEIN.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; P_rich_extensn.
InterPro; IPR002965; P_rich_extensn.
Pfam; PF00041; fn3; 2.
Pfam; PF00047; ig; 2.
PRINTS; PR00014; FMTYPEIII.
PRINTS; PR01217; PRICHEXTENSN.
SMART; SM00060; FN3; 2.
PROCEST: SM00409; IG; 2.
     Sakano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; Southwick A., Davis R.W., "The sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1."; "The sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1."; "InterPro; IPR001623; DnaJ_N.

InterPro; IPR001623; DnaJ_N.

InterPro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 SCSVHDLLLGNP-DYYVCGSTPYTITNRMAAEEVL-----EYGVTYFVCATPNAQPFLER 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAEPVQLGVNQNVRRFSGQTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TASKYS-AASQQVQRNRGNAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTTTLAPLOKSVP----KPSGAPK 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KSAARSELGMYVSKRQEFYLRRARRRRKFAWKPVLQSISEMKPVMEFHTPMAYRDSGSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRSPVQPKPQPLPTPPMETPDKASPNPKRSLSPPNKRQPPPLRKSPTPPEPIKVTPALLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIDNEQLTHEMSYGTSDHALK-----MDVRKSPSLNSADSANKPTTDSSNPKLNLTL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QPKVVHRGSKILPRESKHGVHVRELRSPTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPH 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STTLHDLIEGSEYKFRYKAENPYGLSEPSGESELLFIPDPKRGITKPKSATRIAGDEKDK 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PKNASTPSLPGPKNIS--PPRQVSVPQRSSPPPKNVSP-PPQPAFVA----R 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -PKTGAGGMQVPPR-----RKTLSPPRPQADAST----GMSPKQSPSAKRK-PKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
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IPR003961;
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ilarity 22.4%;
Conservative 4
P_rich_extensn
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FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5;
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Best Local
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Best Local
070495
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lilaca V., Lou A., Young S., Messing J.;
Lilaca V., Lou A., Young S., Messing J.;
"Retroctransposable elements of Sorghum bicolor.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR114171; AAD27567.1;
Interpro; IPR002965; P.rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9XEQ2;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 125.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magonliophyta; Lilopsida; Poales; Poaceae; PACC cl.
Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01217; PRICHEXTENSN. SMART; SM00271; DnaJ; 1. PROSITE; PS50076; DNAJ_2; 1. SEQUENCE 796 AA; 87577 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XEQ2
                                                                                                                                          548
                                                                                     604
                                                                                                 285 PQRS-SPPPKNVSPPPQPAFVARTA-----SKYSAASQQVQRNRGNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 PFPLSQPPSNSKPFPMSQSSQNSKPFPVSQSSQKSKPLLVSQSSQRSK 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 TPNAQ------PFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRK 120
                                          σ
                                                                                PPRSPSPPPRSPTPPPRSPTSKRSAPPPPPPAPPSPKSARSVPSPPKRGSKK
                                                                                                                                     RKRFIIIPQHRDSSNLSPILSPAHHSAAGGDNAGSPPTPAAAKPTLPPP----PPRSPPP 603
                                                                                                                                                               RRKFAWKPVLQSISEMKPVME--FHTPMAYRDSGSPPKNAST-PSLPGPKNISPPRQVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEAAQLSLLPSVSDSS----HASQPTRSNQSHAVSKPQPVSKPHPPFPMSQPPP--TSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QFDQQLLQEQQQASWRQQVGQEHSSGSSGDWKRPVEEVRLINLNNATERVQSSRRFAEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPQSQSQSPQHHQQQSQSPQHPNQNQTVSFQNQQLP-FQLHQPHFAQAVQTQSQSQQQRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PORSSPPPKNVSP-----PPQPAFVARTASKYSAASQQVQRNR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKFAWKPVLQSISEMKPVMEFHTPMAYRDSG----SPPKNASTPSLPGPKNISPPRQVSV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPPSRSFEG----SSHRTPSTELTWASKPTPVSEPVRHSELVPWQYSEPARQYQL--SSRS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESPLPNLSGEALSPTATAKDEIT-----QMILKSAARSEL--GMYVSKRQEFYLRRARRR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VFDYHSVTMQQLESIRNEGPEPHLAGD-----RPSKHLKLVFIRHCLRALRLPRISIDLM 175
                                                                                                                                                                                             37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;83
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                                                                                                                                                                                                                                                               al protein.
1104 AA;
               PRELIMINARY;
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                                                                                                                                                                                                          7.18;
                                                                                                                                                                                                                                                                125894 MW;
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Pred. No. 0.01
36; Mismatches
                                                                                                                                                                                            Score 122.5; DB Pred. No. 0.035; 7; Mismatches
             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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             897
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                                                                                                                                                                                                                      DB 10;
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                                                                                                                                                                                                                                                                CRC64;
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                                                                                                           326
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Best Loc
Matches
Kruse M., Gamulin V.,
Mueller W.E.G.;
"Molecular evolution o
                                                                                                                                                                          062570
062570;
01-AUG-1998
01-AUG-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PLENTY-OF-PROLINES-101.
                                                                                                                                        01-AUG-1998 (TIEMBLEEL 07, Created)
01-AUG-1998 (TIEMBLEEL 07, Last sequence update)
01-DEC-2001 (TIEMBLEEL 19, Last annotation update)
PROTEIN KINASE C-RELATED KINASE (PRKSD).
Suberites domuncula.
Subarryota, Metazoa, Porifera; Demospongiae; Tetract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002483; PWI.
Pfam; PF01480; PWI; 1.
SMART; SM00311; PWI; 1.
SEQUENCE 897 AA; 10116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vayssiere B.M., Camonis J.H.;
Submitted (MAY-1998) to the E
EMBL; AF062655; AAC17422.1; -
MGD; MGI:1858303; Srrm1.
                                         SEQUENCE FROM N.A. MEDLINE-96394688;
                                                                           Submitted
                                                                                      Mueller W.E.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                   NCBI_TaxID-55567;
                                                                                                                                                                                                                                                                                                                                                                                                                                   151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 TPNAQPFLERQ------PKVVH------RGSKI-----LPRFSKH-GVHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match
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                                                                                                                                                                                                                                                                                                                                                                   SPRMQMG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESPSPAPKPRKVELSESEEDKGSKMAAADSVQQRRQYRRQNQQSSSDSGSSSTSEDERPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELRSPT-------HGSQQSR--KVFDYHSVTMQQLESIRNEGPEPHLAGDRPS
                                                                                                                                                                                                                                                                            KRRVSHS
                                                                                                                                                                                                                                                                                                                                   PKNASTPSLPGPKNISP-PRQVSVP-QR---SSPPPK--NVSPPPQPAFVARTASKYSAA
                                                                                                                                                                                                                                                                                                                                                                                        AARSELGMYVSKRQEFYLRRARRRKFAWKPVL - - - QSISEMKPVMEFHTPMAYRDSGSP
                                                                                                                                                                                                                                                                                                                                                                                                               RSHVK-------RGEVGRRRLSPSRSASPSPRKRQKET
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75; Conser
                                                                          (APR-1997)
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nilarity 24.4%;
Conservative 3
                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                            657
                                                                                                                                                                                                                                                                                                                                                                   -KRWQSPVTKSSRRRRSPSPPPARRRRSPSPAPPPPPPPPPPRRRRSPTP
                              PubMed=8798342;
V., Cetkovic H.,
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101166
                                                                                                                                 Porifera; Demospongiae;
tidae; Suberites.
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                                                                          EMBL/GenBank/DDBJ
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          Metazoan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62160BEB6772BD10
                                Pancer
                                                                                                                                                                                                                       1102
        protein
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                                Z . ,
                                                                                                                                           Tetractinomorpha;
            kinase
                                Mueller I.M.,
                                                                           databases
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; Murinae; Mus
         C
          multigene
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RESULT RESULT ID SYSTEM OF SYSTEM OF
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Matches
                                                                                                                                                                                                                                                                       D 09SK28 PRELIMINARY; PRT; 742 AA.

C 09SK28;

C 09SK28;

T 01-MAY-2000 (TrEMBLrel. 13, Created)

T 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

E ARTG25050 PROTEIN.

N ATG25050.

ATG25050:

S Arabidopsis thaliana (Mouse-ear cress).

S Arabidopsis thaliana (Mouse-ear cress).

S Arabidopsis thaliana (Mouse-ear cress).

C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra

Eukaryota; Viridiplantae; Streptophyta; Core eudic

C Eukaryota; Magnoliophyta; eudicotyledons; core eudic

C eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF02185; HR1; 3.
Pfam; PF00433; pkinase_C; 1.
Pfam; PF00433; pkinase_C; 1.
SMART; SM00074; HR1; 3.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00213; S_TK, X; 1.
PROSITE; PS001017; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_T; 1.
PROSITE; PS001108; PROTEIN_KINASE_T; 1.
PROSITE; PS001108; PROTEIN_KINASE_T; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family.";
J. Mol. Evol. 43
-!- SIMILARITY:
STRAINE-CY. COLUMBIA;

MEDLINE-20083487; PubMed=10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.E.

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat

Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y13104; CAA73558.1; HSSP; Q63450; 1A06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1102 AA; 124286 MW; F4F7AD5248323E83 CRC64;
                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAFVARTASKYSAASQQVQRNRGNAKSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PII-PPPREFLGGSVSSTDE---HRVDDNIGPPPKFIMESWSAVSPTHRHTSPQHQKPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAG - - - - DRPSKHLKLVFIRHCLRALRLPRISIDLMESPLPNLSGEALSPTATAKDEITQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRFSKHGVHVRELRSP--THGSQQSRKVFDYHS-----VTMQQLESIRNEGP--EPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGREYNTVISPPPTRPSVPAPTRSPAHQVFPPPPNPSFPTPLS-PSRVAPLPPISQPPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TSGGSTPKSPITPTSPPYFDHSGRKRSLQENGGDL-PPPIP-MSEEDL--IVGAPHSATE
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IPR000961; Pkinase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Y: BELONGS TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -TELNTDIVTWARLLNRSAPSTHTDPHISSPMVISTQDKSSKQESPPHSPH
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25.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SER/THR
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                                                                                                                                                                                                                                                                                                                  eudicots;
                                                                                                                                                                                                                                                                                                                                               Tracheophyta;
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RESULT

Q91Z40

ID Z20

ID Z20

AC Q9

AC Q9

DT 011

TO 01

TO 0
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Best Local S
Matches 60
                                                                                                                      STRAIN=BRISTOL
Wohldmann P., B
"The sequence o
                                                                         Submitted [3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O9TZ40 PRELIMINARY; PRT; 539 AA.
09TZ40;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 62.1 KDA PROTEIN.
w07B3.2.
                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ da
EMBL; AC006585; AAD23008.1; -
InterPro; IPR002965; P_xich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
SEQUENCE 742 AA; 81758 MW; EB5E7A4096F57D28
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=6239;
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lin X.;
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STRAIN-CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLRALRLPRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVFNQITAANILQESLDSGSPRSPDSRSLLESALEKVKEKTKLM-----ISENIVSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PASPSISFLPTLHPLTSSQPKKASPQCPQSPTPVHSNGPPSAEAAVTSSPLPP-LKPLRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDLMESPLPNLSGEALSPTATAKDEITQMILKSAARSELGM-----YVSKRQEFYLRRA
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                                                                                              (OCT-1998)
                                                                                    , Bauer C., Roman
e of C. elegans c
e of C. the f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peloderinae;
                                                                                                                                                                     N2;
                                                                                                                                                                                                                                                                                                                                        PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.6%;
                                                                                      Rohlfing T., Gillam B.;
gans cosmid W07B3.";
the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 114; DB 10;
Pred. No. 0.12;
8; Mismatches 127;
                                                                                                                                                                                                                                                            Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         databases
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Best Loc
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004712;
01-JUL-1997
01-JUL-1997
01-CCT-2000
T10M13 10.
                   EU Arabidopsis sequencing project; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AF001308; AAC78701.1; -. EMBL; AF001535; AAB57800.1; -. EMBL; AL161493; CAB60702.1; -.
                                                                                                                      Spiegel L.A., Huang E.N., Nascimento L. Preston R.R., Matero A., Shah R., O'Sha Shekher M., Schutz K., See L.H., Swaby Mewes H.W., Lemcke K., Mayer K.
                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. LANDSBERG;
Till S., Granat S., Parnell L., Kaplan N., Hoffman J., I
Johnson A.F., Dedhia N., Martienssen R., McCombie W.R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                   Johnson A.F., la Bastide M., Lodhi M.,
Gnoj L., Gottesman T., Granat S., Hamee
Shohdy N., Van Keuren K., Parnell L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Direct Submission.";
Submitted (JUL-2001) to the
EMBL; AF100304; AAC68911.1;
Hypothetical protein.
SEQUENCE 539 AA; 62094 MW
              Hypothetical
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                             Shohdy N.,
McCombie W.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            T10M13.10 OR AGAA.5 OR AT4G02090
                                                                                                                                                                               SEQUENCE FROM
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                                                                                                                                  Huang E.N., Nascimento L.U., de la Bastide M., Matero A., Shah R., O'Shaughnessy A., Rodriguez Chutz K., See L.H., Swaby I., Habermann K., Dedh
22316 MW;
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 CAA7EEDF62FAA8AF CRC64;
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N., Martienssen
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an N., Schutz K
Martienssen R.,
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Q91T14;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Darai G., Bahr U.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF281817; ARX57163.1; -.
SEQUENCE 393 AA; 41784 MW; F48A27BB3C53BDFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21211637; PubMed-11312357;
Bahr U., Daral G.;
"Analysis and Characterization of the Complete Genome of Tupala (Tree Shrew) Herpesvirus.";
"J. Virol. 75:4854-4870(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tupaia herpesvirus.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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NCBI_TaxID-10397;
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                                                                                                                                                                                                                                                                                           83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYGVTYFVCATPNAQPFLERQPKVVHRGSKILPRFSKHGVHVRELRSPTHGSQQSRKVFD 123
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                                                                               --VLKPIEEAVSGL-----
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                                                                                                                            KFAWKPYLQSISEMKPYMEFHTPMAYRDSGSPPKNASTPSLPGPKNISPPRQVSVPQRSS 289
                                                                                                                                                                                                                                                                                           PPPPFDGGDPARHPGTPPPTVTTITVTTVRPPASPPTHAVPRTHRSP-----
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; Pred. No. 0.041;
24; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                           ; Score 109.5; D; Pred. No. 0.13; 25; Mismatches
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InterPro: IPRO00408; RCC1.
InterPro: IPRO00365; Znf_FYVE.
Pfam; PF00363; FYVE; 1.
Pfam; PF00415; RCC1; 6.
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MEDLINE-99397451; PubMed=10470850;
Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
"Sequence features of the regions of 1,011,550 bp covered by seventeen
pl and TAC Clones.";
DNA Res. 6:183-195(1999).
EMBL, AB017067; BAB08447.1; -...
EMBL, AB017067; BAB08447.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS50012; RCC1_3; 6.
SEQUENCE 1073 AA; 116497 MW; 7A9F6C2F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
TMV RESISTANCE PROTEIN-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 PTHGSQQS--RKVFDY------HSVTMQQLESIR----NEGPEPHLAGDRPS 150
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                                                                                  821 ELLNQEVVRLRAQAESL 837
                                                                                                                                  313 -AASQQVQRNRGNAKSL 328
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     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHLKLVFIRHCLRALRLPRISIDLMESPLPNLSGE------ALSPTATAKDEIT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVFTWGKGANGRLGHGDVEDRKAPTLVDALKERHVKNIACGSNFTAAICLH-----KWVS
                                                                                                                                                                                       RGPPKPAVTP-----SSSRPVSPFSRRSSPPRSVTPIPLNVGLGFSTSTAESLKKTN
                                                                                                                                                                                                                                                                                                                                              QMILKSAARSELGMYVSKRQEFYLRRARRRRKFAWKPVLQSISEMKPVMEFHTPMAYRDS
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                                                                                                                                                                                                                                     GSPPKNASTPSLPGPKNISPPRQVSVPQRSSPPPKNVSPPPQ-----PAFVARTASKYS
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89; Conservative
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23.6%; Pred. No. 0.49;
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16;

SORRER REPRESENTATIONS OF THE PROPERTY OF THE

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RESULT
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Best Local :
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Q9UHAB;
01-MAY-2000 (TrEMBLrel. 13, C.
01-MAY-2000 (TrEMBLrel. 13, L.
01-DEC-2001 (TrEMBLrel. 19, L.
SPLICING COACTIVATOR SUBUNIT:
SRM300.
                                                                                                                                                                                                                                                                                                                                                                                                             Q9M2X4 PRELIMINARY; PRT; 651 AA. Q9M2X4; Q9M2X4; Q1-QCT-2000 (TrEMBLrel. 15, Created) Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update) Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update) HYPOTHETICAL 72.3 KDA PROTEIN.
                                                                                                                                                                                                                                                                           T16K5.190.

Arabidopsis thaliana (Mouse-ear cress).

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosid

Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
                                           EU Arabidopsis sequencing project;
Submitted (JAN-2000) to the EMBL/G
EMBL; AL132965; CAB66922.1; -
                                                                                                                                                 SEQUENCE FROM N.A.
Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
Rewes H.W., Lemcke K., Mayer K.F.X., Quetter F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                            Hypothetical
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. PubMed=10668804;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Primates;
  72344 MW;
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                                                                    EMBL/GenBank/DDBJ
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Pred. No. 1.3;
27; Mismatches
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CRC64;
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                                                                                                                                                                                                                                                                                                                              Rosidae;
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RESULT
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Best Local
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Virus Res. 65:21-32(1999).
EMBL; Y17753; CAC03567.1; -
InterPro; IPR003124; WH2.
Pfam; PF02205; WH2; 2.
SMART; SM00246; WH2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9EEF8;
Q9EEF8;
01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                MEDLINE-20033815; PubMed-10564750; Chen X., Ijkel W.F.J., Dominy C., Faktor O., Hayakawa T., Wang C.H.,
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=92268862; PubMed=1588315;
Zanotto P.M., Sampaio M.J., Johnson D.W., Rocha T.L., Maruniak J.E.;
"The Anticarsia gemmatalis nuclear polyhedrosis virus polyhedrin genuregion: sequence analysis, gene product and structural comparisons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat
HYPOTHETICAL P60 PROTEIN.
                                                              Helicoperva
                                                                                         Vlak J.M.;
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                        Zanotto P.M.A., Kessing B.D., Maruniak "Phylogenetic interrelationships among rates and host associations.";
                                                                                                                                                                                                                                MEDLINE=94044871;
                                                                                                                                                                                                                                             STRAIN=2D;
                                                                                                                                                                                                                                                                             Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                               Zanotto
                                                                                                                                                                                                                                                                                                            STRAIN=2D;
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                                                                                                                                                                                                                                                                                                                                             region: sequence analysis, gene pr
J. Gen. Virol. 73:1049-1056(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=31507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anticarsia gemmatalis nuclear polyhedrosis virus (AgMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                         'Identification, sequence analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562
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                                                                                                                                                                                 Invertebr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLRRARRRKFAWKPVLQSISEMKPVMEFHTPM----AYRDSGSPPKNASTPS-LPGPKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SISRKLLAQRIYEQDDETESCS------PGLIHATSFASPLPRGSNKKLRTVPLS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RVRYKERNKPSDKSITEKKKKMSYQDPQHPVSAPPPQGYPPKEGYPPAGYPPPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALK ----- ELVSSPEEGSSGSE --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALRLPRISIDLMESPLPNLSGEALSPTATAKDEITQMILKSAAR---SELGMYVSKRQEF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESDIFPSSFHKTPEGRR----KLTKEELQKFTKESTE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                           tion, sequence analysis and phylogeny of the armigera single-nucleocapsid baculovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPTHGSQQSRKVFDYHSVTMQQLESIRNEGPEPHLAGDRPSKHLKLVFIRHCLR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                       N.A.
                                                                                                                                                                               Pathol.
                                                                                                                                                                                                                              PubMed=8228320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.3%;
22.5%;
                                                                                                Dominy C., Z
                                                                                                                                                                              62:147-164(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 109;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                Zanotto P.M.A., Premumkar A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -NVSPPPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  517
                                                                                                                                                                                                                  ч
                                                                                                                                                                                                       baculoviruses:
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.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --KQAARGTSEPVGECTKKKKQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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                                                                                                Hashimoto
Krell P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                     Evolutionary
                                                                         lef-2
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Hu
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                                                                                                                                                                                                                                                                                                    Query Match 6.2%; Score 108; DB 12; Length 517; Best Local Similarity 20.9%; Pred. No. 0.26; Matches 73; Conservative 40; Mismatches 102; Indels 134; Gaps
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                 236 YP------LKH------FYLSPHQ--HLHPLRHLHRHLWHPHLLLQNRRNPRV 274
                                                                                                                   188 SPTATAKDEITQMILKSAARSELGMYVSKRQEEYLRRARRRRKFAMKPVLQSISEMKPVM 247
                                                                                                                                                                                                      152 RPHOLRLYLKORKRLWCLHLHPLKRLOYLHFSLH-KHLHPLNRLOH-----FHPL 200
                                                                                                                                                                                                                                                      275 REQLOKVRCLAARLTNLNTLLELALMDKPKTSVPPKPPHLSKANSMEVGDKIAPPEGTNT 334
                                                                            248 EFH-----TPMAYRDSGSPPKNAST 267
                                                                                                                                                                                                                            73 ATPNAOPFLEROPKV----VHRGSKI-LPRFSKHGVHVRELRSPTHGSOOSRKVFDYHSV 127
                                                                                                                                                                                                                                                                                                                                                                     517 AA; 59000 MW; B50872BBF3633995 CRC64;
                                                                                                                                                                                                                                                                                                          15;
```

Search completed: September 16, 2002, 00:51:11 Job time: 475 sec



PubMed Entrez BLAST OMIM Taxonomy Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Mitogen-activated protein kinase 12 (Extracellular

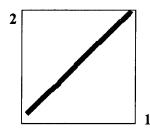
Sequence 1 gi 2851522 signal-regulated kinase 6) (ERK-6) (ERK5) (Stress-activated protein kinase-3) (Mitogen-activated protein kinase p38 gamma) (MAP kinase p38 gamma).

Length  $367 \frac{(1...)}{367}$ 

Sequence 2 gi 1136298 WIPK [Nicotiana tabacum]

Length 375  $\frac{(1...)}{375}$ 





NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 292 bits (747), Expect = 5e-78
Identities = 149/339 (43%), Positives = 219/339 (63%), Gaps = 8/339 (2%)



Query: 21 WEVRAVYRD-LQPVGSGAYGAVCSAVDGRTGAKVAIKKLYRPFQSELFAKRAYRELRLLK 79
+E+ YR + P+G GAYG VCS ++ VA+KK+ F + AKR RE++LL+

Sbjct: 36 FEITTKYRPPIMPIGRGAYGIVCSVLNTELNEMVAVKKIANAFDIYMDAKRTLREIKLLR 95

Query: 80 HMRHENVIGLLDVFTPDETLDDFTDFYLVMPFMGTDLGKLMK-HEKLGEDRIQFLVYQML 138

H+ HENVIGL DV P +F+D Y+ M TDL ++++ ++ L ED Q+ +YQ+L Sbjct: 96 HLDHENVIGLRDVIPPP-LRREFSDVYIATELMDTDLHQIIRSNQGLSEDHCQYFMYQLL 154

abjec: 36 HPD4EWA1GPKDA1555-PKKEt2DA11M1FPMD1DP4611K2N6GP2ED4C61tW16PF 124

Query: 139 KGLRYIHAAGIIHRDLKPGNLAVNEDCELKILDFGLARQ--ADSEMTGYVVTRWYRAPEV 196 +GL+YIH+A ++HRDLKP NL VN +C+LKI DFGLAR + MT YVVTRWYRAPE+

Sbjct: 155 RGLKYIHSANVLHRDLKPSNLLVNANCDLKICDFGLARPNIENENMTEYVVTRWYRAPEL 214

Query: 197 ILNWMRYTQTVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMKVTGTPPAEFVQRLQSD 256 +LN YT +D+WSVGCI E++ K LF G DH+ Q++ + ++ GTP + LQ++

Sbjct: 215 LLNSSDYTAAIDVWSVGCIFMELMNRKPLFGGKDHVHQIRLLTELLGTPTEADLGFLQNE 274

Query: 257 EAKNYMKGLPELEKKDFASILTNASPLAVNLLEKMLVLDAEQRVTAGEALAHPYFESLHD 316

Query: 257 EAKNYMKGLPELEKKDFASILTNASPLAVNLLEKMLVLDAEQRVTAGEALAHPYFESLHD 316 +AK Y++ LP+ ++ A + ++PLA++L++KML D +R+T EAL HPY LHD

 ${\tt Sbjct:\ 275\ DAKRYIRQLPQHPRQQLAEVFPHVNPLAIDLVDKMLTFDPTRRITVEEALDHPYLAKLHD\ 334}$ 

Query: 317 TEDEPQVQKYDDSFDDVDRTL--DEWKRVTYKEVLSFKP 353

DEP + SFD + + ++ K + Y+E LS P

Sbjct: 335 AGDEP-ICPVPFSFDFEQQGIGEEQIKDMIYQEALSLNP 372

CPU time: 0.08 user secs. 0.01 sys. secs 0.09 total secs.

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S1: 41 (21.8 bits) S2: 60 (27.7 bits)

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Lambda
           ĸ
                 Н
            0.137
   0.320
                     0.405
Gapped
Lambda
           K
                 Η
   0.267
           0.0410
                     0.140
Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 1022
Number of Sequences: 0
Number of extensions: 86
Number of successful extensions: 4
Number of sequences better than 300.0: 1
Number of HSP's better than 300.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 367
length of database: 330,426,180
effective HSP length: 123
effective length of query: 244
effective length of database: 219,683,991
effective search space: 53602893804
effective search space used: 53602893804
T: 9
A: 40
X1: 16 ( 7.4 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
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9/16/02 3·54 PM

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